

Sequence Listing

<110> Avi J. Ashkenazi  
Kevin P. Baker  
David Botstein  
Luc Desnoyers  
Dan L. Eaton  
Napoleone Ferrara  
Sherman Fong  
Wei-Qiang Gao  
Hanspeter Gerber  
Mary E. Gerritsen  
Audrey Goddard  
Paul J. Godowski  
Austin L. Gurney  
Ivar J. Kljavin  
Jennie P. Mather  
Mary A. Napier  
James Pan  
Nicholas F. Paoni  
Margaret Ann Roy  
Timothy A. Stewart  
Daniel Tumas  
Colin K. Watanabe  
P. Mickey Williams  
William I. Wood  
Zemin Zang

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65														75
Tyr	Cys	Arg	Gln	Gly	Tyr	Tyr	Leu	Gln	Met	His	Pro	Asp	Gly	Ala
80														90
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95														105
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110														120
Thr	Gly	Leu	Tyr	Ile	Ala	Met	Asn	Gly	Glu	Gly	Tyr	Leu	Tyr	Pro
125														135
Ser	Glu	Leu	Phe	Thr	Pro	Glu	Cys	Lys	Phe	Lys	Glu	Ser	Val	Phe
140														150
Glu	Asn	Tyr	Tyr	Val	Ile	Tyr	Ser	Ser	Met	Leu	Tyr	Arg	Gln	Gln
155														165
Glu	Ser	Gly	Arg	Ala	Trp	Phe	Leu	Gly	Leu	Asn	Lys	Glu	Gly	Gln
170														180
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185														195
Phe	Leu	Pro	Lys	Pro	Leu	Glu	Val	Ala	Met	Tyr	Arg	Glu	Pro	Ser
200														210
Leu	His	Asp	Val	Gly	Glu	Thr	Val	Pro	Lys	Pro	Gly	Val	Thr	Pro
215														225
Ser	Lys	Ser	Thr	Ser	Ala	Ser	Ala	Ile	Met	Asn	Gly	Gly	Lys	Pro
230														240
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 <211> 2609  
 <212> DNA  
 <213> Homo Sapien

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 ttgtttaaca tacttagaaa atgaagtgtt catttttaac attcctcc 200

caattggttt aatgctgaat tactgaagag ggctaagcaa aaccaggtgc 250  
ttgcgctgag ggctctgcag tggctggag gacccggcg ctctccccgt 300  
gtcctctcca cgactcgctc ggccctctg gaataaaaca cccgcgagcc 350  
ccgagggccc agaggaggcc gacgtgccc agtcctccg ggggtcccgc 400  
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<212> PRT  
<213> Homo Sapien

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Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu  
35 40 45  
Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val  
50 55 60

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Tyr	Arg	Gly	Pro	Tyr	Ser	Asn	Pro	Tyr	Ser	Thr	Pro	Tyr	Ser	Gly
80									85				90	
Pro	Tyr	Pro	Ala	Ala	Ala	Pro	Pro	Leu	Ser	Ala	Pro	Asn	Tyr	Pro
95									100				105	
Thr	Ile	Ser	Arg	Pro	Leu	Ile	Cys	Arg	Phe	Gly	Tyr	Gln	Met	Asp
110									115				120	
Glu	Ser	Asn	Gln	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	Thr	Asp	Ser
125									130				135	
His	Gln	Cys	Asn	Pro	Thr	Gln	Ile	Cys	Ile	Asn	Thr	Glu	Gly	Gly
140									145				150	
Tyr	Thr	Cys	Ser	Cys	Thr	Asp	Gly	Tyr	Trp	Leu	Leu	Glu	Gly	Gln
155									160				165	
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170									175				180	
Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	Ser	Cys	Thr	Cys	Asn	Pro	Gly
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Phe	Thr	Leu	Asn	Glu	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val	Asn	Glu
200									205				210	
Cys	Ala	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr	Tyr
215									220				225	
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230									235				240	
Asp	Gly	Val	His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Ser	Glu
245									250				255	
Phe	Leu	Cys	Gln	His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Thr	Tyr	Phe
260									265				270	
Cys	Ser	Cys	Pro	Pro	Gly	Tyr	Ile	Leu	Leu	Asp	Asp	Asn	Arg	Ser
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Asp	Pro	Ile	Arg	Cys	Glu	Glu	Pro	Tyr	Leu	Arg	Ile	Ser	Asp	Asn
320									325				330	
Arg	Cys	Met	Cys	Pro	Ala	Glu	Asn	Pro	Gly	Cys	Arg	Asp	Gln	Pro
335									340				345	
Phe	Thr	Ile	Leu	Tyr	Arg	Asp	Met	Asp	Val	Val	Ser	Gly	Arg	Ser

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365	370	375
Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg		
380	385	390
Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val		
395	400	405
Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu		
410	415	420
Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser		
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 <212> DNA  
 <213> Homo Sapien

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 <211> 428  
 <212> PRT  
 <213> Homo Sapien  
  
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     20                  25                  30  
 Phe Gln Ile Ala Asp Cys Ala Tyr Arg Asp Leu Glu Ser Val Pro  
     35                  40                  45  
 Pro Gly Phe Pro Ala Asn Val Thr Thr Leu Ser Leu Ser Ala Asn  
     50                  55                  60  
 Arg Leu Pro Gly Leu Pro Glu Gly Ala Phe Arg Glu Val Pro Leu  
     65                  70                  75  
 Leu Gln Ser Leu Trp Leu Ala His Asn Glu Ile Arg Thr Val Ala  
     80                  85                  90  
 Ala Gly Ala Leu Ala Ser Leu Ser His Leu Lys Ser Leu Asp Leu  
     95                  100                 105  
 Ser His Asn Leu Ile Ser Asp Phe Ala Trp Ser Asp Leu His Asn  
   110                  115                 120  
 Leu Ser Ala Leu Gln Leu Leu Lys Met Asp Ser Asn Glu Leu Thr  
   125                  130                 135  
 Phe Ile Pro Arg Asp Ala Phe Arg Ser Leu Arg Ala Leu Arg Ser  
   140                  145                 150  
 Leu Gln Leu Asn His Asn Arg Leu His Thr Leu Ala Glu Gly Thr  
   155                  160                 165  
 Phe Thr Pro Leu Thr Ala Leu Ser His Leu Gln Ile Asn Glu Asn  
   170                  175                 180  
 Pro Phe Asp Cys Thr Cys Gly Ile Val Trp Leu Lys Thr Trp Ala  
   185                  190                 195  
 Leu Thr Thr Ala Val Ser Ile Pro Glu Gln Asp Asn Ile Ala Cys  
   200                  205                 210  
 Thr Ser Pro His Val Leu Lys Gly Thr Pro Leu Ser Arg Leu Pro  
   215                  220                 225

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245									250				255	
His	Cys	Asp	Val	Asp	Gly	Gln	Pro	Ala	Pro	Gln	Leu	His	Trp	His
260									265				270	
Ile	Gln	Ile	Pro	Ser	Gly	Ile	Val	Glu	Ile	Thr	Ser	Pro	Asn	Val
275									280				285	
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290									295				300	
Gln	Pro	Arg	Phe	Gln	Ala	Phe	Ala	Asn	Gly	Ser	Leu	Leu	Ile	Pro
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320									325				330	
Asn	Glu	Leu	Gly	Ser	Ala	Glu	Ser	Ser	Val	Asp	Val	Ala	Leu	Ala
335									340				345	
Thr	Pro	Gly	Glu	Gly	Glu	Asp	Thr	Leu	Gly	Arg	Arg	Phe	His	
350									355				360	
Gly	Lys	Ala	Val	Glu	Gly	Lys	Gly	Cys	Tyr	Thr	Val	Asp	Asn	Glu
365									370				375	
Val	Gln	Pro	Ser	Gly	Pro	Glu	Asp	Asn	Val	Val	Ile	Ile	Tyr	Leu
380									385				390	
Ser	Arg	Ala	Gly	Asn	Pro	Glu	Ala	Ala	Val	Ala	Glu	Gly	Val	Pro
395									400				405	
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 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<210> 19  
 <211> 22  
 <212> DNA  
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220  
223 Synthetic oligonucleotide probe  
400 19  
ccaatgtgtg caagcggttg tg 22  
210 20  
211 50  
212 DNA  
213 Artificial Sequence  
220  
223 Synthetic oligonucleotide probe  
400 20  
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210 21  
211 2033  
212 DNA  
213 Homo Sapien  
400 21  
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attggcttga agcaatataa tatattgtaa aaaaaacaca gctcttacct 1950  
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<210> 22  
<211> 379  
<212> PRT  
<213> Homo Sapien

<400> 22  
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Pro	Gln	Glu	Glu	Ser	Leu	Tyr	Leu	Trp	Ile	Asp	Ala	His	Gln	Ala
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Arg	Val	Leu	Ile	Gly	Phe	Glu	Glu	Asp	Ile	Leu	Ile	Val	Ser	Glu
					50				55				60	
Gly	Lys	Met	Ala	Pro	Phe	Thr	His	Asp	Phe	Arg	Lys	Ala	Gln	Gln
					65				70				75	
Arg	Met	Pro	Ala	Ile	Pro	Val	Asn	Ile	His	Ser	Met	Asn	Phe	Thr
					80				85				90	
Trp	Gln	Ala	Ala	Gly	Gln	Ala	Glu	Tyr	Phe	Tyr	Glu	Phe	Leu	Ser
					95				100				105	
Leu	Arg	Ser	Leu	Asp	Lys	Gly	Ile	Met	Ala	Asp	Pro	Thr	Val	Asn
					110				115				120	
Val	Pro	Leu	Leu	Gly	Thr	Val	Pro	His	Lys	Ala	Ser	Val	Val	Gln
					125				130				135	
Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln	Asp	Gly	Val	Ala	Ala	Phe
					140				145				150	
Glu	Val	Asp	Val	Ile	Val	Met	Asn	Ser	Glu	Gly	Asn	Thr	Ile	Leu
					155				160				165	
Gln	Thr	Pro	Gln	Asn	Ala	Ile	Phe	Phe	Lys	Thr	Cys	Gln	Gln	Ala
					170				175				180	
Glu	Cys	Pro	Gly	Gly	Cys	Arg	Asn	Gly	Gly	Phe	Cys	Asn	Glu	Arg
					185				190				195	
Arg	Ile	Cys	Glu	Cys	Pro	Asp	Gly	Phe	His	Gly	Pro	His	Cys	Glu
					200				205				210	
Lys	Ala	Leu	Cys	Thr	Pro	Arg	Cys	Met	Asn	Gly	Gly	Leu	Cys	Val
					215				220				225	
Thr	Pro	Gly	Phe	Cys	Ile	Cys	Pro	Pro	Gly	Phe	Tyr	Gly	Val	Asn
					230				235				240	
Cys	Asp	Lys	Ala	Asn	Cys	Ser	Thr	Thr	Cys	Phe	Asn	Gly	Gly	Thr
					245				250				255	
Cys	Phe	Tyr	Pro	Gly	Lys	Cys	Ile	Cys	Pro	Pro	Gly	Leu	Glu	Gly
					260				265				270	
Glu	Gln	Cys	Glu	Ile	Ser	Lys	Cys	Pro	Gln	Pro	Cys	Arg	Asn	Gly
					275				280				285	
Gly	Lys	Cys	Ile	Gly	Lys	Ser	Lys	Cys	Lys	Cys	Ser	Lys	Gly	Tyr
					290				295				300	
Gln	Gly	Asp	Leu	Cys	Ser	Lys	Pro	Val	Cys	Glu	Pro	Gly	Cys	Gly
					305				310				315	
Ala	His	Gly	Thr	Cys	His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu

320 325 330  
Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu  
335 340 345  
Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr  
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Pro Ser Leu Lys Lys Ala Glu Glu Arg Arg Asp Pro Pro Glu Ser  
365 370 375  
Asn Tyr Ile Trp

<210> 23  
<211> 783  
<212> DNA  
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<210> 24  
<211> 94  
<212> PRT  
<213> Homo Sapien

<400> 24

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35 40 45  
Trp Val Arg Ser Tyr Glu Phe Thr Ser Asn Ser Cys Ser Gln Arg  
50 55 60  
Ala Val Ile Phe Thr Thr Lys Arg Gly Lys Lys Val Cys Thr His  
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<210> 25  
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<212> DNA  
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<223> Synthetic oligonucleotide probe  
  
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<210> 28  
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<212> DNA  
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<210> 29  
 <211> 386  
 <212> PRT  
 <213> Homo Sapien

<400> 29

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								20		25			30	
Trp	Leu	Leu	Asp	Pro	Lys	Ile	Leu	Lys	Phe	Val	Val	Phe	Ile	Val
								35		40			45	
Ala	Val	Leu	Leu	Pro	Val	Arg	Val	Asp	Ser	Ala	Thr	Ile	Pro	Arg
								50		55			60	
Gln	Asp	Glu	Val	Pro	Gln	Gln	Thr	Val	Ala	Pro	Gln	Gln	Arg	
								65		70			75	
Arg	Ser	Leu	Lys	Glu	Glu	Glu	Cys	Pro	Ala	Gly	Ser	His	Arg	Ser
								80		85			90	
Glu	Tyr	Thr	Gly	Ala	Cys	Asn	Pro	Cys	Thr	Glu	Gly	Val	Asp	Tyr
								95		100			105	
Thr	Ile	Ala	Ser	Asn	Asn	Leu	Pro	Ser	Cys	Leu	Leu	Cys	Thr	Val
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<210> 30  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<210> 31  
<211> 963  
<212> DNA  
<213> Homo Sapien

<400> 31  
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agagctcatt ccagatgcac ccctgtccag tgctgcctat agcatccgca 150  
gcatcgggga gaggcctgtc ctcaaagctc cagtcgggaa aaggcaaaaa 200  
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ctgaataacg atgccaagaa tgccatagaa gcacttgaa gtaaagaaat 550  
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<210> 32  
<211> 235  
<212> PRT  
<213> Homo Sapien

<400> 32

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			20					25					30	
Leu	Ile	Pro	Asp	Ala	Pro	Leu	Ser	Ser	Ala	Ala	Tyr	Ser	Ile	Arg
				35				40					45	
Ser	Ile	Gly	Glu	Arg	Pro	Val	Leu	Lys	Ala	Pro	Val	Pro	Lys	Arg
				50				55					60	
Gln	Lys	Cys	Asp	His	Trp	Thr	Pro	Cys	Pro	Ser	Asp	Thr	Tyr	Ala
				65				70					75	
Tyr	Arg	Leu	Leu	Ser	Gly	Gly	Arg	Ser	Lys	Tyr	Ala	Lys	Ile	
			80					85					90	
Cys	Phe	Glu	Asp	Asn	Leu	Leu	Met	Gly	Glu	Gln	Leu	Gly	Asn	Val
				95				100					105	
Ala	Arg	Gly	Ile	Asn	Ile	Ala	Ile	Val	Asn	Tyr	Val	Thr	Gly	Asn
				110					115				120	
Val	Thr	Ala	Thr	Arg	Cys	Phe	Asp	Met	Tyr	Glu	Gly	Asp	Asn	Ser
				125				130					135	
Gly	Pro	Met	Thr	Lys	Phe	Ile	Gln	Ser	Ala	Ala	Pro	Lys	Ser	Leu
				140				145					150	
Leu	Phe	Met	Val	Thr	Tyr	Asp	Asp	Gly	Ser	Thr	Arg	Leu	Asn	Asn
				155				160					165	
Asp	Ala	Lys	Asn	Ala	Ile	Glu	Ala	Leu	Gly	Ser	Lys	Glu	Ile	Arg
				170				175					180	
Asn	Met	Lys	Phe	Arg	Ser	Ser	Trp	Val	Phe	Ile	Ala	Ala	Lys	Gly
				185				190					195	
Leu	Glu	Leu	Pro	Ser	Glu	Ile	Gln	Arg	Glu	Lys	Ile	Asn	His	Ser
				200				205					210	
Asp	Ala	Lys	Asn	Asn	Arg	Tyr	Ser	Gly	Trp	Pro	Ala	Glu	Ile	Gln
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<400>	33													
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<210> 34  
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<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 34  
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<210> 35  
<211> 18  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 35  
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<210> 36  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 36  
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<210> 37  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 37  
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<210> 38  
<211> 1215  
<212> DNA  
<213> Homo Sapien

<400> 38  
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<210> 39  
<211> 330  
<212> PRT  
<213> Homo Sapien

<400> 39  
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Phe Val Ala Leu Pro Ala Ser Gly Trp Leu Thr Thr Gly Ala Pro  
20 25 30  
Glu Pro Pro Pro Leu Ser Gly Ala Pro Gln Asp Gly Ile Arg Ile  
35 40 45  
Asn Val Thr Thr Leu Lys Asp Asp Gly Asp Ile Ser Lys Gln Gln

50	55	60
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65	70	75
Asp Leu Pro Val Asn Ser Gly Val Thr Arg Ile Ser Cys Gln Thr		
80	85	90
Leu Ile Val Lys Asn Glu Asn Leu Glu Asn Leu Glu Glu Lys Glu		
95	100	105
Tyr Phe Gly Ile Val Ser Val Arg Ile Leu Val His Glu Trp Pro		
110	115	120
Met Thr Ser Gly Ser Ser Leu Gln Leu Ile Val Ile Gln Glu Glu		
125	130	135
Val Val Glu Ile Asp Gly Lys Gln Val Gln Gln Lys Asp Val Thr		
140	145	150
Glu Ile Asp Ile Leu Val Lys Asn Arg Gly Val Leu Arg His Ser		
155	160	165
Asn Tyr Thr Leu Pro Leu Glu Glu Ser Met Leu Tyr Ser Ile Ser		
170	175	180
Arg Asp Ser Asp Ile Leu Phe Thr Leu Pro Asn Leu Ser Lys Lys		
185	190	195
Glu Ser Val Ser Ser Leu Gln Thr Thr Ser Gln Tyr Leu Ile Arg		
200	205	210
Asn Val Glu Thr Thr Val Asp Glu Asp Val Leu Pro Gly Lys Leu		
215	220	225
Pro Glu Thr Pro Leu Arg Ala Glu Pro Pro Ser Ser Tyr Lys Val		
230	235	240
Met Cys Gln Trp Met Glu Lys Phe Arg Lys Asp Leu Cys Arg Phe		
245	250	255
Trp Ser Asn Val Phe Pro Val Phe Phe Gln Phe Leu Asn Ile Met		
260	265	270
Val Val Gly Ile Thr Gly Ala Ala Val Val Ile Thr Ile Leu Lys		
275	280	285
Val Phe Phe Pro Val Ser Glu Tyr Lys Gly Ile Leu Gln Leu Asp		
290	295	300
Lys Val Asp Val Ile Pro Val Thr Ala Ile Asn Leu Tyr Pro Asp		
305	310	315
Gly Pro Glu Lys Arg Ala Glu Asn Leu Glu Asp Lys Thr Cys Ile		
320	325	330

<210> 40  
<211> 2498

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 279 280 281 282 283 284 285 286 287 288 289 289 290 291 292 293 294 295 296 297 298 299 299 300 301 302 303 304 305 306 307 308 309 309 310 311 312 313 314 315 316 317 318 319 319 320 321 322 323 324 325 326 327 328 329 329 330 331 332 333 334 335 336 337 338 339 339 340 341 342 343 344 345 346 347 348 349 349 350 351 352 353 354 355 356 357 358 359 359 360 361 362 363 364 365 366 367 368 369 369 370 371 372 373 374 375 376 377 378 379 379 380 381 382 383 384 385 386 387 388 389 389 390 391 392 393 394 395 396 397 398 399 399 400

<212> DNA  
<213> Homo Sapien

<400> 40  
cgtctctgcg ttcgccatgc gtcccggggc gccagggcca ctctggcctc 50  
tgccctgggg ggccctggct tggccgtgg gcttcgttag ctccatgggc 100  
tcggggaaacc ccgcgcggc tgggtttgc tggctccagc agggccagga 150  
ggccacctgc agcctggtgc tccagactga tgtcacccgg gccgagtgct 200  
gtgcctccgg caacattgac accgcctggt ccaacctcac ccacccgggg 250  
aacaagatca acctcctcgg cttcttggc cttgtccact gccttccctg 300  
caaagattcg tgcgacggcg tggagtgcgg cccgggcaag gcgtgcccga 350  
tgctgggggg ccgccccggc tgcgagtgcg cgcccgactg ctcggggctc 400  
ccggcgccgc tgcaggtctg cggctcagac ggcccaccc accgcgacga 450  
gtgcgagctg cgccgcgcgc gctgcccgg ccacccggac ctgagcgtca 500  
tgtaccgggg ccgctgcccgc aagtctgtg agcacgtggt gtgcccggc 550  
ccacagtctg gctcgctgga ccagacgggc agcgcact gcgtggtgtg 600  
tcgagcggcg ccctgcccgt tgccctccag cccggccag gagctttgcg 650  
gcaacaacaa cgtcacctac atctcctctg gccacatgcg ccaggccacc 700  
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cacccctgag gagccgcag gtggtagtc tgcagaagag gaagagaact 800  
tcgtgtgagc ctgcaggaca ggcctggcc tggcccga ggccccccat 850  
catcccctgt tatttattgc cacagcagag tctaatttat atgccacgga 900  
caactccttag agcccgatt cggaccactt gggatccca gaacctccct 950  
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gagggctggg cattctctgc tggtaattcc tgaagaggca tgactgttt 1200  
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tatggaggat ctagcctggg tgagtatgga gggtagcc tgggtgagta 1400  
 tggagggtct agcctgggtg tgtatggagg gtctagcctg ggtgagtatg 1450  
 gagggtctag cctgggtgtg tatggagggt ctagcctggg tgagtatgga 1500  
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 caagaaggct gccaccatcc cctgccagcc caagaactcc agttccccca 1650  
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 ggcggggacc acgggccact gtcacccac tggcccccggag ggggggtgttag 1950  
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 ccagtggcac cactaggtgc ctgctgcctc cacagtgggg ttcacacacca 2050  
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 ctcctccagc ccccaggcag tgccttacct gtggtgccca gaaaagtgcc 2400  
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<210> 41  
 <211> 263  
 <212> PRT  
 <213> Homo Sapien

<400> 41  
 Met Arg Pro Gly Ala Pro Gly Pro Leu Trp Pro Leu Pro Trp Gly  
 1 5 10 15  
 Ala Leu Ala Trp Ala Val Gly Phe Val Ser Ser Met Gly Ser Gly  
 20 25 30

Asn	Pro	Ala	Pro	Gly	Gly	Val	Cys	Trp	Leu	Gln	Gln	Gly	Gln	Glu
35									40					45
Ala	Thr	Cys	Ser	Leu	Val	Leu	Gln	Thr	Asp	Val	Thr	Arg	Ala	Glu
50									55					60
Cys	Cys	Ala	Ser	Gly	Asn	Ile	Asp	Thr	Ala	Trp	Ser	Asn	Leu	Thr
65									70					75
His	Pro	Gly	Asn	Lys	Ile	Asn	Leu	Leu	Gly	Phe	Leu	Gly	Leu	Val
80									85					90
His	Cys	Leu	Pro	Cys	Lys	Asp	Ser	Cys	Asp	Gly	Val	Glu	Cys	Gly
95									100					105
Pro	Gly	Lys	Ala	Cys	Arg	Met	Leu	Gly	Gly	Arg	Pro	Arg	Cys	Glu
110									115					120
Cys	Ala	Pro	Asp	Cys	Ser	Gly	Leu	Pro	Ala	Arg	Leu	Gln	Val	Cys
125									130					135
Gly	Ser	Asp	Gly	Ala	Thr	Tyr	Arg	Asp	Glu	Cys	Glu	Leu	Arg	Ala
140									145					150
Ala	Arg	Cys	Arg	Gly	His	Pro	Asp	Leu	Ser	Val	Met	Tyr	Arg	Gly
155									160					165
Arg	Cys	Arg	Lys	Ser	Cys	Glu	His	Val	Val	Cys	Pro	Arg	Pro	Gln
170									175					180
Ser	Cys	Val	Val	Asp	Gln	Thr	Gly	Ser	Ala	His	Cys	Val	Val	Cys
185									190					195
Arg	Ala	Ala	Pro	Cys	Pro	Val	Pro	Ser	Ser	Pro	Gly	Gln	Glu	Leu
200									205					210
Cys	Gly	Asn	Asn	Asn	Val	Thr	Tyr	Ile	Ser	Ser	Cys	His	Met	Arg
215									220					225
Gln	Ala	Thr	Cys	Phe	Leu	Gly	Arg	Ser	Ile	Gly	Val	Arg	His	Ala
230									235					240
Gly	Ser	Cys	Ala	Gly	Thr	Pro	Glu	Glu	Pro	Pro	Gly	Gly	Glu	Ser
245									250					255
Ala	Glu	Glu	Glu	Glu	Asn	Phe	Val							
260														
<210> 42														
<211> 20														
<212> DNA														
<213> Artificial Sequence														
<220>														
<223> Synthetic oligonucleotide probe														
<400> 42														
tcctgtgagc acgtggtg 20														

<210> 43  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 43  
gggtgggata gacctgcg 18

<210> 44  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 44  
aaggccaaga aggctgcc 18

<210> 45  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 45  
ccaggcctgc agacccag 18

<210> 46  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 46  
cttcctcagt ctttccagga tatac 24

<210> 47  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 47  
aagctggata tcctccgtgt tgtc 24

<210> 48  
<211> 27  
<212> DNA

<213> Artificial Sequence  
  
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<223> Synthetic oligonucleotide probe  
  
<400> 48  
cctgaagagg catgactgct tttctca 27  
  
<210> 49  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 49  
ggggataaaac ctattaatta ttgctac 27  
  
<210> 50  
<211> 44  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 50  
aacgtcacct acatctcctc gtgccacatg cgccaggcca cctg 44  
  
<210> 51  
<211> 1690  
<212> DNA  
<213> Homo Sapien  
  
<400> 51  
tgcagagctt gtggaggcca tggggcgcggt cgtcgcggag ctcgtctcct 50  
cgctgctggg gttgtggctg ttgctgtgca gctgcggatg ccccgagggc 100  
gccgagctgc gtgctccgcc agataaaaatc gcgattattt gagccggaat 150  
tggtggcact tcagcagcct attacctgcg gcagaaaattt gggaaaatgt 200  
tgaagataga cctgtttgaa agagaagagg tcggggcccg cctggctacc 250  
atgatggtgc aggggcaaga atacgaggca ggaggttctg tcatccatcc 300  
tttaaatctg cacatgaaac gttttgtcaa agacctgggt ctctctgctg 350  
ttcaggcctc tggtggccta ctggggatataatggaga gactctggta 400  
tttggggaga gcaactgggtt cataattaac gtgattaaat tagttggcg 450  
ctatggattt caatccctcc gtatgcacat gtgggttagag gacgtgttag 500  
acaaggatcat gaggatctac cgctaccagt ctcataacta tgccttcagt 550

agtgtcgaaa aattacttca tgctctagga ggagatgact tccttggaaat 600  
gcttaatcga acacttcttg aaaccttgca aaaggccgac ttttctgaga 650  
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agcacggaca tcaatgcctt tgtggggcgt gtgtcactgt cctgttctga 750  
ttctggcctt tggcagtag aaggtggcaa taaacttgtt tgctcagggc 800  
ttctgcaggc atccaaaagc aatcttatat ctggctcagt aatgtacatc 850  
gaggagaaaa caaagaccaa gtacacagga aatccaacaa agatgtatga 900  
agtggtctac caaattggaa ctgagactcg ttcagacttc tatgacatcg 950  
tcttggtggc cactccgttg aatcgaaaaa tgtcgaatat tactttctc 1000  
aactttgatc ctccaattga ggaattccat caatattatc aacatatagt 1050  
gacaacttta gttaaggggg aattgaatac atctatctt agctctagac 1100  
ccatagataa atttggcctt aatacagttt taaccactga taattcagat 1150  
ttgttcattt acagtattgg gattgtgccc tctgtgagag aaaaggaaga 1200  
tcctgagcca tcaacagatg gaacatatgt ttggaagatc ttttcccaag 1250  
aaactcttac taaagcacaa attttaaagc tctttctgtc ctatgattat 1300  
gctgtgaaga agccatggct tgcatatcct cactataagc ccccgagaa 1350  
atgcccctct atcattctcc atgatcgact ttattacctc aatggcatag 1400  
agtgtgcagc aagtgcacatg gagatgagtg ccattgcagc ccacaacgct 1450  
gcactccttg cctatcaccg ctggAACGGG cacacagaca tgattgatca 1500  
ggatggctta tatgagaaac ttaaaactga actatgaagt gacacactcc 1550  
ttttccctt cctagttcca aatgactatc agtggcaaaa aagaacaaaa 1600  
tctgagcaga gatgatttg aaccagatat tttgccatta tcattgttta 1650  
ataaaaagtaa tccctgctgg tcataaggaaa aaaaaaaaaa 1690

<210> 52  
<211> 505  
<212> PRT  
<213> Homo Sapien

<400> 52  
Met Gly Arg Val Val Ala Glu Leu Val Ser Ser Leu Leu Gly Leu  
1 5 10 15  
Trp Leu Leu Leu Cys Ser Cys Gly Cys Pro Glu Gly Ala Glu Leu  
20 25 30

Arg	Ala	Pro	Pro	Asp	Lys	Ile	Ala	Ile	Ile	Gly	Ala	Gly	Ile	Gly	
						35				40			45		
Gly	Thr	Ser	Ala	Ala	Tyr	Tyr	Leu	Arg	Gln	Lys	Phe	Gly	Lys	Asp	
						50			55			60			
Val	Lys	Ile	Asp	Leu	Phe	Glu	Arg	Glu	Glu	Val	Gly	Gly	Arg	Leu	
						65			70			75			
Ala	Thr	Met	Met	Val	Gln	Gly	Gln	Glu	Tyr	Glu	Ala	Gly	Gly	Ser	
						80			85			90			
Val	Ile	His	Pro	Leu	Asn	Leu	His	Met	Lys	Arg	Phe	Val	Lys	Asp	
						95			100			105			
Leu	Gly	Leu	Ser	Ala	Val	Gln	Ala	Ser	Gly	Gly	Leu	Leu	Gly	Ile	
						110			115			120			
Tyr	Asn	Gly	Glu	Thr	Leu	Val	Phe	Glu	Glu	Ser	Asn	Trp	Phe	Ile	
						125			130			135			
Ile	Asn	Val	Ile	Lys	Leu	Val	Trp	Arg	Tyr	Gly	Phe	Gln	Ser	Leu	
						140			145			150			
Arg	Met	His	Met	Trp	Val	Glu	Asp	Val	Leu	Asp	Lys	Phe	Met	Arg	
						155			160			165			
Ile	Tyr	Arg	Tyr	Gln	Ser	His	Asp	Tyr	Ala	Phe	Ser	Ser	Val	Glu	
						170			175			180			
Lys	Leu	Leu	His	Ala	Leu	Gly	Gly	Asp	Asp	Phe	Leu	Gly	Met	Leu	
						185			190			195			
Asn	Arg	Thr	Leu	Leu	Glu	Thr	Leu	Gln	Lys	Ala	Gly	Phe	Ser	Glu	
						200			205			210			
Lys	Phe	Leu	Asn	Glu	Met	Ile	Ala	Pro	Val	Met	Arg	Val	Asn	Tyr	
						215			220			225			
Gly	Gln	Ser	Thr	Asp	Ile	Asn	Ala	Phe	Val	Gly	Ala	Val	Ser	Leu	
						230			235			240			
Ser	Cys	Ser	Asp	Ser	Gly	Leu	Trp	Ala	Val	Glu	Gly	Gly	Asn	Lys	
						245			250			255			
Leu	Val	Cys	Ser	Gly	Leu	Leu	Gln	Ala	Ser	Lys	Ser	Asn	Leu	Ile	
						260			265			270			
Ser	Gly	Ser	Val	Met	Tyr	Ile	Glu	Glu	Lys	Thr	Lys	Thr	Lys	Tyr	
						275			280			285			
Thr	Gly	Asn	Pro	Thr	Lys	Met	Tyr	Glu	Val	Val	Tyr	Gln	Ile	Gly	
						290			295			300			
Thr	Glu	Thr	Arg	Ser	Asp	Phe	Tyr	Asp	Ile	Val	Leu	Val	Ala	Thr	
						305			310			315			
Pro	Leu	Asn	Arg	Lys	Met	Ser	Asn	Ile	Thr	Phe	Leu	Asn	Phe	Asp	

320	325	330
Pro Pro Ile Glu Glu Phe His Gln Tyr Tyr Gln His Ile Val Thr		
335	340	345
Thr Leu Val Lys Gly Glu Leu Asn Thr Ser Ile Phe Ser Ser Arg		
350	355	360
Pro Ile Asp Lys Phe Gly Leu Asn Thr Val Leu Thr Thr Asp Asn		
365	370	375
Ser Asp Leu Phe Ile Asn Ser Ile Gly Ile Val Pro Ser Val Arg		
380	385	390
Glu Lys Glu Asp Pro Glu Pro Ser Thr Asp Gly Thr Tyr Val Trp		
395	400	405
Lys Ile Phe Ser Gln Glu Thr Leu Thr Lys Ala Gln Ile Leu Lys		
410	415	420
Leu Phe Leu Ser Tyr Asp Tyr Ala Val Lys Lys Pro Trp Leu Ala		
425	430	435
Tyr Pro His Tyr Lys Pro Pro Glu Lys Cys Pro Ser Ile Ile Leu		
440	445	450
His Asp Arg Leu Tyr Tyr Leu Asn Gly Ile Glu Cys Ala Ala Ser		
455	460	465
Ala Met Glu Met Ser Ala Ile Ala Ala His Asn Ala Ala Leu Leu		
470	475	480
Ala Tyr His Arg Trp Asn Gly His Thr Asp Met Ile Asp Gln Asp		
485	490	495
Gly Leu Tyr Glu Lys Leu Lys Thr Glu Leu		
500	505	

<210> 53  
 <211> 728  
 <212> DNA  
 <213> Homo Sapien

<400> 53  
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 cagtttcttc caaccttgcc attgcaataa aaaaggaaaa gaggcctcct 150  
 cagacactct caagaggatg gggagatgac atcacttggg tacaaaactta 200  
 tgaagaaggt ctctttatg ctcaaaaaag taagaagcca ttaatggta 250  
 ttcatcacct ggaggattgt caatactctc aagcactaaa gaaagtat 300  
 gccccaaatg aagaaataca agaaatggct cagaataagt tcatacatgct 350

aaaccttatg catgaaacca ctgataagaa tttatcacct gatgggcaat 400  
 atgtgcctag aatcatgttt gtagaccctt cttAACAGT tagAGCTGAC 450  
 atAGCTGGAA gataCTCTAA cAGATTGTC ACATATGAGC CTCGGGATT 500  
 ACCCCTATTG ATAGAAAACA TGAAGAAAGC ATTAAGACTT ATTCAGTCAG 550  
 AGCTATAAGA GATGATGGAA AAAAGCCTTC ACTTCAAAGA AGTCAAATT 600  
 CATGAAGAAA ACCTCTGGCA CATTGACAAA TACTAAATGT GCAAGTATAT 650  
 AGATTTGTA ATATTACTAT TTAGTTTTT TAATGTGTTT GCAATAGTCT 700  
 TATTAATAAATA AATGTTTTT AAATCTGA 728

<210> 54  
 <211> 166  
 <212> PRT  
 <213> Homo Sapien

<400> 54  
 Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Leu Val Thr  
 1 5 10 15

Val Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro  
 20 25 30

Pro Gln Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val  
 35 40 45

Gln Thr Tyr Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys  
 50 55 60

Pro Leu Met Val Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln  
 65 70 75

Ala Leu Lys Lys Val Phe Ala Gln Asn Glu Glu Ile Gln Glu Met  
 80 85 90

Ala Gln Asn Lys Phe Ile Met Leu Asn Leu Met His Glu Thr Thr  
 95 100 105

Asp Lys Asn Leu Ser Pro Asp Gly Gln Tyr Val Pro Arg Ile Met  
 110 115 120

Phe Val Asp Pro Ser Leu Thr Val Arg Ala Asp Ile Ala Gly Arg  
 125 130 135

Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu Pro Arg Asp Leu Pro Leu  
 140 145 150

Leu Ile Glu Asn Met Lys Lys Ala Leu Arg Leu Ile Gln Ser Glu  
 155 160 165

Leu

<210> 55  
 <211> 537  
 <212> DNA  
 <213> Homo Sapien

<400> 55  
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 gcgtcagaga gaaagaactg actgaaacgt ttgagatgaa gaaagttctc 100  
 ctcctgatca cagccatctt ggcagtggct gttggttcc cagtctctca 150  
 agaccagggaa cgagaaaaaa gaagtatcg tgacagcgt gaatttagctt 200  
 cagggttttt tgggttttcc tacccatatac catttcgccc acttccacca 250  
 attccatttc caagatttc atggttttaga cgttaatttc ctattccaat 300  
 acctgaatct gcccctacaa cttcccttcc tagcgaaaag taaacaagaa 350  
 ggataagtcg cgtaaaacctt ggtcacctga aattgaaatt gagccacttc 400  
 cttgaagaat caaaaattcct gttataaaaa gaaaaacaaa tgtaattgaa 450  
 atagcacacacatgcattctca gtcaatatct ttagtgatct tctttaataa 500  
 acatgaaaagc aaagattttg gtttcttaat ttccaca 537

<210> 56  
 <211> 85  
 <212> PRT  
 <213> Homo Sapien

<400> 56  
 Met Lys Lys Val Leu Leu Ile Thr Ala Ile Leu Ala Val Ala  
 1 5 10 15

Val Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser  
 20 25 30

Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro  
 35 40 45

Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg  
 50 55 60

Phe Pro Trp Phe Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser  
 65 70 75

Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys  
 80 85

<210> 57  
 <211> 2997  
 <212> DNA  
 <213> Homo Sapien

<400> 57

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gctcgccctg gcccgcggcg ccgcgggagc gccgggcccc gacggtttag 150  
acgtctgtgc cacttgccat gaacatgcca catgccagca aagagaaggg 200  
aagaagatct gtatttgc当地 ctatggattt gtagggAACg ggaggactca 250  
gtgtgtt当地 aaaaatgagt gccagtttgg agccactctt gtctgtgggaa 300  
accacacatc ttgccacaac acccccgggg gcttctattt cattgcctg 350  
gaaggatatc gagccacaaa caacaacaag acattcattc ccaacgatgg 400  
cacctttgt acagacatag atgagtgtga agtttctggc ctgtgcaggc 450  
atggagggcg atgcgtgaac actcatgggaa gcttgaatg ctactgtatg 500  
gatggatact tgccaaggaa tggacctgaa ccttccacc cgaccaccga 550  
tgccacatca tgcacagaaa tagactgtgg taccctctt gaggttccag 600  
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tatgcttgca gagaaggatt ctgcgtgtt ccagaagata cagttcaag 700  
ctgcacagggc ctggcacat gggagtcccc aaaattacat tgccaagaga 750  
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cacagctcca ggctggcg ggctggctcgc tatgtctgtc aagagggttt 850  
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gtgcctgttag tgtgtttggaa tctgtaccct acgactgatt atacgggtgaa 1450

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 <212> PRT  
 <213> Homo Sapien  
 <400> 58  
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     20                         25                         30  
 Pro Gly Pro Asp Gly Leu Asp Val Cys Ala Thr Cys His Glu His  
     35                         40                         45  
 Ala Thr Cys Gln Gln Arg Glu Gly Lys Lys Ile Cys Ile Cys Asn  
     50                         55                         60  
 Tyr Gly Phe Val Gly Asn Gly Arg Thr Gln Cys Val Asp Lys Asn  
     65                         70                         75  
 Glu Cys Gln Phe Gly Ala Thr Leu Val Cys Gly Asn His Thr Ser  
     80                         85                         90  
 Cys His Asn Thr Pro Gly Gly Phe Tyr Cys Ile Cys Leu Glu Gly  
     95                         100                         105  
 Tyr Arg Ala Thr Asn Asn Asn Lys Thr Phe Ile Pro Asn Asp Gly  
   110                         115                         120  
 Thr Phe Cys Thr Asp Ile Asp Glu Cys Glu Val Ser Gly Leu Cys  
   125                         130                         135  
 Arg His Gly Gly Arg Cys Val Asn Thr His Gly Ser Phe Glu Cys  
   140                         145                         150  
 Tyr Cys Met Asp Gly Tyr Leu Pro Arg Asn Gly Pro Glu Pro Phe  
   155                         160                         165  
 His Pro Thr Thr Asp Ala Thr Ser Cys Thr Glu Ile Asp Cys Gly  
   170                         175                         180  
 Thr Pro Pro Glu Val Pro Asp Gly Tyr Ile Ile Gly Asn Tyr Thr  
   185                         190                         195  
 Ser Ser Leu Gly Ser Gln Val Arg Tyr Ala Cys Arg Glu Gly Phe  
   200                         205                         210  
 Phe Ser Val Pro Glu Asp Thr Val Ser Ser Cys Thr Gly Leu Gly  
   215                         220                         225  
 Thr Trp Glu Ser Pro Lys Leu His Cys Gln Glu Ile Asn Cys Gly  
   230                         235                         240

Asn	Pro	Pro	Glu	Met	Arg	His	Ala	Ile	Leu	Val	Gly	Asn	His	Ser
245									250				255	
Ser	Arg	Leu	Gly	Gly	Val	Ala	Arg	Tyr	Val	Cys	Gln	Glu	Gly	Phe
260									265				270	
Glu	Ser	Pro	Gly	Gly	Lys	Ile	Thr	Ser	Val	Cys	Thr	Glu	Lys	Gly
275									280				285	
Thr	Trp	Arg	Glu	Ser	Thr	Leu	Thr	Cys	Thr	Glu	Ile	Leu	Thr	Lys
290									295				300	
Ile	Asn	Asp	Val	Ser	Leu	Phe	Asn	Asp	Thr	Cys	Val	Arg	Trp	Gln
305									310				315	
Ile	Asn	Ser	Arg	Arg	Ile	Asn	Pro	Lys	Ile	Ser	Tyr	Val	Ile	Ser
320									325				330	
Ile	Lys	Gly	Gln	Arg	Leu	Asp	Pro	Met	Glu	Ser	Val	Arg	Glu	Glu
335									340				345	
Thr	Val	Asn	Leu	Thr	Thr	Asp	Ser	Arg	Thr	Pro	Glu	Val	Cys	Leu
350									355				360	
Ala	Leu	Tyr	Pro	Gly	Thr	Asn	Tyr	Thr	Val	Asn	Ile	Ser	Thr	Ala
365									370				375	
Pro	Pro	Arg	Arg	Ser	Met	Pro	Ala	Val	Ile	Gly	Phe	Gln	Thr	Ala
380									385				390	
Glu	Val	Asp	Leu	Leu	Glu	Asp	Asp	Gly	Ser	Phe	Asn	Ile	Ser	Ile
395									400				405	
Phe	Asn	Glu	Thr	Cys	Leu	Lys	Leu	Asn	Arg	Arg	Ser	Arg	Lys	Val
410									415				420	
Gly	Ser	Glu	His	Met	Tyr	Gln	Phe	Thr	Val	Leu	Gly	Gln	Arg	Trp
425									430				435	
Tyr	Leu	Ala	Asn	Phe	Ser	His	Ala	Thr	Ser	Phe	Asn	Phe	Thr	Thr
440									445				450	
Arg	Glu	Gln	Val	Pro	Val	Val	Cys	Leu	Asp	Leu	Tyr	Pro	Thr	Thr
455									460				465	
Asp	Tyr	Thr	Val	Asn	Val	Thr	Leu	Leu	Arg	Ser	Pro	Lys	Arg	His
470									475				480	
Ser	Val	Gln	Ile	Thr	Ile	Ala	Thr	Pro	Pro	Ala	Val	Lys	Gln	Thr
485									490				495	
Ile	Ser	Asn	Ile	Ser	Gly	Phe	Asn	Glu	Thr	Cys	Leu	Arg	Trp	Arg
500									505				510	
Ser	Ile	Lys	Thr	Ala	Asp	Met	Glu	Glu	Met	Tyr	Leu	Phe	His	Ile
515									520				525	
Trp	Gly	Gln	Arg	Trp	Tyr	Gln	Lys	Glu	Phe	Ala	Gln	Glu	Met	Thr

530	535	540
Phe Asn Ile Ser Ser Ser Arg Asp	Pro Glu Val Cys Leu Asp	
545	550	555
Leu Arg Pro Gly Thr Asn Tyr Asn Val	Ser Leu Arg Ala Leu Ser	
560	565	570
Ser Glu Leu Pro Val Val Ile Ser Leu	Thr Thr Gln Ile Thr Glu	
575	580	585
Pro Pro Leu Pro Glu Val Glu Phe Phe	Thr Val His Arg Gly Pro	
590	595	600
Leu Pro Arg Leu Arg Leu Arg Lys Ala	Lys Glu Lys Asn Gly Pro	
605	610	615
Ile Ser Ser Tyr Gln Val Leu Val Leu	Pro Leu Ala Leu Gln Ser	
620	625	630
Thr Phe Ser Cys Asp Ser Glu Gly Ala	Ser Ser Phe Phe Ser Asn	
635	640	645
Ala Ser Asp Ala Asp Gly Tyr Val Ala	Ala Glu Leu Leu Ala Lys	
650	655	660
Asp Val Pro Asp Asp Ala Met Glu Ile	Pro Ile Gly Asp Arg Leu	
665	670	675
Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro	Leu Lys Arg Gly Ser Asp	
680	685	690
Tyr Cys Ile Ile Leu Arg Ile Thr Ser	Glu Trp Asn Lys Val Arg	
695	700	705
Arg His Ser Cys Ala Val Trp Ala Gln	Val Lys Asp Ser Ser Leu	
710	715	720
Met Leu Leu Gln Met Ala Gly Val Gly	Leu Gly Ser Leu Ala Val	
725	730	735
Val Ile Ile Leu Thr Phe Leu Ser Phe	Ser Ala Val	
740	745	

<210> 59

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

ccacttgccca tgaacatgcc ac 22

<210> 60

<211> 25

<212> DNA

213 Artificial Sequence  
220  
223 Synthetic oligonucleotide probe  
400 60  
cctcttgaca gacatagcga gccac 25  
210 61  
211 43  
212 DNA  
213 Artificial Sequence  
220  
223 Synthetic oligonucleotide probe  
400 61  
caactcttgc tggggaaacc acacatcttgc acacactgtt ggc 43  
210 62  
211 2015  
212 DNA  
213 Homo Sapien  
400 62  
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gagcagacac tgcgtatgaca acggacgaca cagaagtgcgc cgctatgact 200  
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acatctccca acttcatggt gctgatgcgc acctccgtgg agacatcagc 400  
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tcacatccac cggagtgtat gatatgggag gggcttcacc tggtccccaga 1900  
ggtgtccttg gactcacctt ggcacatgtt ctgtgtttca gtaaagagag 1950  
acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttcactcagt 2000  
gtggcccaaa aaaaaa 2015

<210> 63  
<211> 482  
<212> PRT  
<213> Homo Sapien

<400> 63  
Met Gly Cys Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys  
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Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg

20	25	30
Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala		
35	40	45
Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu		
50	55	60
Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile		
65	70	75
Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg		
80	85	90
Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu		
95	100	105
Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu		
110	115	120
Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro		
125	130	135
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu		
140	145	150
Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr		
155	160	165
Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser		
170	175	180
Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser		
185	190	195
Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg		
200	205	210
Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile		
215	220	225
Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu		
230	235	240
Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile		
245	250	255
Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp		
260	265	270
Ile Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser		
275	280	285
Asp Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile		
290	295	300
Thr Glu Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr		
305	310	315

Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro
320														330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr
335														345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu
350														360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val
365														375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly
380														390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro
395														405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr
410														420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro
425														435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr
440														450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met
455														465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro
470														480

Gln Thr

<210> 64  
<211> 1252  
<212> DNA  
<213> Homo Sapien

<400> 64  
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gccactccag aggccatgct tcgtttcttg ccagatttgg ctttcagctt 100  
cctgttaatt ctggctttgg gccaggcagt ccaatttcaa gaatatgtct 150  
ttctccaatt tctgggctta gataaggcgc cttcacccca gaagttccaa 200  
cctgtgcctt atatcttcaa gaaaatttgc caggatcgcg aggcagcagc 250  
gaccactggg gtctcccgag acttatgcta cgtaaaggag ctgggcgtcc 300  
gcgggaatgt acttcgctt ctcctgcctg cagaagctcc tctacttcaa 350  
aagaaaaattt cccaaatcc tcctgcctg cagaagctcc tctacttcaa 400

cctgtctgcc atcaaagaaa gggAACAGTT gacATTGGCC cAGCTGGCC 450  
tggacttggg gcccattct tactataacc tgggaccaga gctggaactg 500  
gctctgttcc tggttcagga gcctcatgtg tggggccaga ccacccctaa 550  
gccaggtaaa atgtttgtgt tgcggtcagt cccatggcca caaggtgctg 600  
ttcacttcaa cctgctggat gtagctaagg attggaatga caaccccccgg 650  
aaaaatttcg ggttattcct ggagatactg gtcaaagaag atagagactc 700  
aggggtgaat tttcagcctg aagacacctg tgccagacta agatgctccc 750  
ttcatgcttc cctgctggtg gtgactctca accctgatca gtgccaccct 800  
tctcgaaaaa ggagagcagc catccctgtc cccaaGCTTT cttgtaaagaa 850  
cctctgccac cgtcaccagc tattcattaa cttccgggac ctgggttggc 900  
acaagtggat cattcccccc aaggggttca tggcaaattt ctgccatgga 950  
gagtgtccct tctcaactgac catctctctc aacagctcca attatgcttt 1000  
catgcaagcc ctgatgcatg ccgttgaccc agagatcccc caggctgtgt 1050  
gtatccccac caagctgtct cccatttcca tgctctacca ggacaataat 1100  
gacaatgtca ttctacgaca ttatgaagac atggtagtcg atgaatgtgg 1150  
gtgtggtag gatgtcagaa atggaaatag aaggagtgaa cttaggtaa 1200  
atcttttaat aaaactacct atctggttta tgaccactta gatcgaaatg 1250

tc 1252

<210> 65  
<211> 364  
<212> PRT  
<213> Homo Sapien

<400> 65  
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20 25 30  
Gln Phe Leu Gly Leu Asp Lys Ala Pro Ser Pro Gln Lys Phe Gln  
35 40 45  
Pro Val Pro Tyr Ile Leu Lys Ile Phe Gln Asp Arg Glu Ala  
50 55 60  
Ala Ala Thr Thr Gly Val Ser Arg Asp Leu Cys Tyr Val Lys Glu  
65 70 75  
Leu Gly Val Arg Gly Asn Val Leu Arg Phe Leu Pro Asp Gln Gly

80	85	90
Phe Phe Leu Tyr Pro Lys Lys Ile Ser Gln Ala Ser Ser Cys Leu		
95	100	105
Gln Lys Leu Leu Tyr Phe Asn Leu Ser Ala Ile Lys Glu Arg Glu		
110	115	120
Gln Leu Thr Leu Ala Gln Leu Gly Leu Asp Leu Gly Pro Asn Ser		
125	130	135
Tyr Tyr Asn Leu Gly Pro Glu Leu Glu Leu Ala Leu Phe Leu Val		
140	145	150
Gln Glu Pro His Val Trp Gly Gln Thr Thr Pro Lys Pro Gly Lys		
155	160	165
Met Phe Val Leu Arg Ser Val Pro Trp Pro Gln Gly Ala Val His		
170	175	180
Phe Asn Leu Leu Asp Val Ala Lys Asp Trp Asn Asp Asn Pro Arg		
185	190	195
Lys Asn Phe Gly Leu Phe Leu Glu Ile Leu Val Lys Glu Asp Arg		
200	205	210
Asp Ser Gly Val Asn Phe Gln Pro Glu Asp Thr Cys Ala Arg Leu		
215	220	225
Arg Cys Ser Leu His Ala Ser Leu Leu Val Val Thr Leu Asn Pro		
230	235	240
Asp Gln Cys His Pro Ser Arg Lys Arg Arg Ala Ala Ile Pro Val		
245	250	255
Pro Lys Leu Ser Cys Lys Asn Leu Cys His Arg His Gln Leu Phe		
260	265	270
Ile Asn Phe Arg Asp Leu Gly Trp His Lys Trp Ile Ile Ala Pro		
275	280	285
Lys Gly Phe Met Ala Asn Tyr Cys His Gly Glu Cys Pro Phe Ser		
290	295	300
Leu Thr Ile Ser Leu Asn Ser Ser Asn Tyr Ala Phe Met Gln Ala		
305	310	315
Leu Met His Ala Val Asp Pro Glu Ile Pro Gln Ala Val Cys Ile		
320	325	330
Pro Thr Lys Leu Ser Pro Ile Ser Met Leu Tyr Gln Asp Asn Asn		
335	340	345
Asp Asn Val Ile Leu Arg His Tyr Glu Asp Met Val Val Asp Glu		
350	355	360
Cys Gly Cys Gly		

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<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
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<223> Synthetic oligonucleotide probe  
  
<400> 66  
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<210> 67  
<211> 47  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 67  
tctccaaattt ctgggcttag ataaggcgcc ttcaccccaag aagttcc 47  
  
<210> 68  
<211> 24  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 68  
gtcccaggtt atagtaagaa ttgg 24  
  
<210> 69  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 69  
gtgttgcgtt cagtcctatg 20  
  
<210> 70  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 70  
gctgtctccc atttccatgc 20  
  
<210> 71  
<211> 24  
<212> DNA

<213> Artificial Sequence  
<220>  
<223> Synthetic oligonucleotide probe  
<400> 71  
cgactaccat gtcttcataa tgtc 24  
  
<210> 72  
<211> 2849  
<212> DNA  
<213> Homo Sapien  
  
<400> 72  
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ggtcgcagag acctcggaga ccgcgcgggg gagacggagg tgctgtgggt 100  
gggggggacc tggctgtct cgtaccgcgc cccaccctcc tcttctgcac 150  
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tgtgcacgc cccggacctg gcccggagga ggcttggccg gcgggagatg 250  
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 <213> Homo Sapien  
 <400> 73  
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     20                  25                  30  
 Gln Gly Glu Gln Gln Glu Trp Glu Gly Thr Glu Glu Leu Pro Ser  
     35                  40                  45  
 Pro Pro Asp His Ala Glu Arg Ala Glu Glu Gln His Glu Lys Tyr  
     50                  55                  60  
 Arg Pro Ser Gln Asp Gln Gly Leu Pro Ala Ser Arg Cys Leu Arg  
     65                  70                  75  
 Cys Cys Asp Pro Gly Thr Ser Met Tyr Pro Ala Thr Ala Val Pro  
     80                  85                  90  
 Gln Ile Asn Ile Thr Ile Leu Lys Gly Glu Lys Gly Asp Arg Gly  
     95                  100                 105  
 Asp Arg Gly Leu Gln Gly Lys Tyr Gly Lys Thr Gly Ser Ala Gly  
   110                  115                 120  
 Ala Arg Gly His Thr Gly Pro Lys Gly Gln Lys Gly Ser Met Gly  
   125                  130                 135  
 Ala Pro Gly Glu Arg Cys Lys Ser His Tyr Ala Ala Phe Ser Val  
   140                  145                 150  
 Gly Arg Lys Lys Pro Met His Ser Asn His Tyr Tyr Gln Thr Val  
   155                  160                 165  
 Ile Phe Asp Thr Glu Phe Val Asn Leu Tyr Asp His Phe Asn Met  
   170                  175                 180  
 Phe Thr Gly Lys Phe Tyr Cys Tyr Val Pro Gly Leu Tyr Phe Phe  
   185                  190                 195  
 Ser Leu Asn Val His Thr Trp Asn Gln Lys Glu Thr Tyr Leu His

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Ile Met Lys Asn Glu Glu Glu Val Val	Ile Leu Phe Ala Gln Val	
215	220	225
Gly Asp Arg Ser Ile Met Gln Ser Gln	Ser Leu Met Leu Glu Leu	
230	235	240
Arg Glu Gln Asp Gln Val Trp Val Arg	Leu Tyr Lys Gly Glu Arg	
245	250	255
Glu Asn Ala Ile Phe Ser Glu Glu Leu Asp	Thr Tyr Ile Thr Phe	
260	265	270
Ser Gly Tyr Leu Val Lys His Ala Thr Glu Pro		
275	280	

<210> 74  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 74  
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<210> 75  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 75  
 ctgaagaagt agaggccggg cacg 24

<210> 76  
 <211> 45  
 <212> DNA  
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<220>  
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<210> 77  
 <211> 1042  
 <212> DNA  
 <213> Homo Sapien

<400> 77  
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tcaggccaca gacggacatg gctgctcaag gctggtccat gtcctgctg 150  
gctgtcctta acctaggcat ctgcgtccgt ccctgtgaca ctcaagagct 200  
acgatgtctg tgtattcagg aacactctga attcattcct ctcaaactca 250  
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tccatgggtg aaggtactg ttggcccaat tactaacagg ttcctacctg 400  
aggaccta acaaaaaggaa ttccacccgg caatgaagct tctgtatagt 450  
gtttagcatg aaaagcctct atatcttca tttgggagac ctgagaacaa 500  
gagaatattt cccttccaa ttcccggagac ctctagacac tttgctgatt 550  
tagctcacaa cagtatagg aattttctac gggactccag tgaagtcagc 600  
ttgacaggca gtgatgccta aaagccactc atgaggcaaa gagtttcaag 650  
gaagctctcc ttctggagtt ttggcggtct cattcttata ctctattccc 700  
gcgttagtct ggtgtatgga tctatgagct ctctttat attttattat 750  
aaatgtttta ttacttaac ttccctagtga atgttcacag gtgactgctc 800  
ccccatcccc atttcttgat attacatata atggcatcat atacccttt 850  
attgactgac aaactactca gattgcttaa cattttgtgc ttcaaagtct 900  
tatcccactc cactatggc ttttacagag tgcattctgg ttttagagcaa 950  
ggctccttgt ctcaagtgc ccagggtgaa atacttctt gaaaaatttt 1000  
cattcatcag aaaatctgaa ataaaaatat gtcttaattt ag 1042

<210> 78  
<211> 167  
<212> PRT  
<213> Homo Sapien

<400> 78  
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20 25 30  
Leu Cys Ile Gln Glu His Ser Glu Phe Ile Pro Leu Lys Leu Ile  
35 40 45  
Lys Asn Ile Met Val Ile Phe Glu Thr Ile Tyr Cys Asn Arg Lys  
50 55 60

Glu	Val	Ile	Ala	Val	Pro	Lys	Asn	Gly	Ser	Met	Ile	Cys	Leu	Asp
65														75
Pro	Asp	Ala	Pro	Trp	Val	Lys	Ala	Thr	Val	Gly	Pro	Ile	Thr	Asn
80														90
Arg	Phe	Leu	Pro	Glu	Asp	Leu	Lys	Gln	Lys	Glu	Phe	Pro	Pro	Ala
95														105
Met	Lys	Leu	Leu	Tyr	Ser	Val	Glu	His	Glu	Lys	Pro	Leu	Tyr	Leu
110														120
Ser	Phe	Gly	Arg	Pro	Glu	Asn	Lys	Arg	Ile	Phe	Pro	Phe	Pro	Ile
125														135
Arg	Glu	Thr	Ser	Arg	His	Phe	Ala	Asp	Leu	Ala	His	Asn	Ser	Asp
140														150
Arg	Asn	Phe	Leu	Arg	Asp	Ser	Ser	Glu	Val	Ser	Leu	Thr	Gly	Ser
155														165

Asp Ala

<210> 79  
<211> 798  
<212> DNA  
<213> Homo Sapien  
  
<220>  
<221> unsure  
<222> 794  
<223> unknown base  
  
<400> 79  
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cctcaagtac agccaaagga agattccgc caaggttgc cgcagctacc 150  
ggaagcagga accaagctta ggctgctcca tccagctat cctgttcttg 200  
ccccgcaagc gctctcaggc agagctatgt gcagacccaa aggagctctg 250  
ggtcagcag ctgatgcagc atctggacaa gacaccatcc ccacagaaac 300  
cagcccaggg ctgcaggaag gacagggggg cctccaagac tggcaagaaa 350  
ggaaagggct ccaaaggctg caagaggact gagcggtcac agacccctaa 400  
agggccatag cccagtgagc agcctggagc cttggagacc ccaccagcct 450  
caccagcgct tgaagcctga acccaagatg caagaaggag gctatgctca 500  
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 <210> 80  
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 <212> PRT  
 <213> Homo Sapien  
  
 <400> 80  
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     20                  25                  30  
 Cys Cys Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val  
     35                  40                  45  
 Arg Ser Tyr Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro  
     50                  55                  60  
 Ala Ile Leu Phe Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys  
     65                  70                  75  
 Ala Asp Pro Lys Glu Leu Trp Val Gln Gln Leu Met Gln His Leu  
     80                  85                  90  
 Asp Lys Thr Pro Ser Pro Gln Lys Pro Ala Gln Gly Cys Arg Lys  
     95                  100                  105  
 Asp Arg Gly Ala Ser Lys Thr Gly Lys Lys Gly Lys Gly Ser Lys  
   110                  115                  120  
 Gly Cys Lys Arg Thr Glu Arg Ser Gln Thr Pro Lys Gly Pro  
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 <210> 81  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 81  
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 <210> 82  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Synthetic oligonucleotide probe

<400> 82  
gaccgcctaaa gggccatag 19

<210> 83  
<211> 924  
<212> DNA  
<213> Homo Sapien

<400> 83  
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cggtctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150  
gtttccaaga aatcaaaaga gccatccaag ctaaggacac cttcccaa 200  
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250  
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cacccctgt gcggtttact gtgggagaca gcccaccttg aaggggaagg 650  
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ataaaattcca tattttacccat atga 924

<210> 84  
<211> 177  
<212> PRT  
<213> Homo Sapien

<400> 84  
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20								25				30		
Ser	Thr	Asp	Met	His	His	Ile	Glu	Glu	Ser	Phe	Gln	Glu	Ile	Lys
35							40					45		
Arg	Ala	Ile	Gln	Ala	Lys	Asp	Thr	Phe	Pro	Asn	Val	Thr	Ile	Leu
50								55				60		
Ser	Thr	Leu	Glu	Thr	Leu	Gln	Ile	Ile	Lys	Pro	Leu	Asp	Val	Cys
65							70					75		
Cys	Val	Thr	Lys	Asn	Leu	Leu	Ala	Phe	Tyr	Val	Asp	Arg	Val	Phe
80								85				90		
Lys	Asp	His	Gln	Glu	Pro	Asn	Pro	Lys	Ile	Leu	Arg	Lys	Ile	Ser
95								100				105		
Ser	Ile	Ala	Asn	Ser	Phe	Leu	Tyr	Met	Gln	Lys	Thr	Leu	Arg	Gln
110								115				120		
Cys	Gln	Glu	Gln	Arg	Gln	Cys	His	Cys	Arg	Gln	Glu	Ala	Thr	Asn
125								130				135		
Ala	Thr	Arg	Val	Ile	His	Asp	Asn	Tyr	Asp	Gln	Leu	Glu	Val	His
140								145				150		
Ala	Ala	Ala	Ile	Lys	Ser	Leu	Gly	Glu	Leu	Asp	Val	Phe	Leu	Ala
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<210> 85  
 <211> 2137  
 <212> DNA  
 <213> Homo Sapien

<400> 85  
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 gtcgcccggcc agcctcccgcc accccccatcg ccggagctgc gccgagagcc 450  
 ccagggaggt gccatgcgga gcgggtgtgt ggtggtccac gtatggatcc 500

tggccggcct ctggctggcc gtggccgggc gccccctcgc cttctcgac 550  
gcggggccccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600  
cctgtacacc tccggccccc acgggctctc cagctgcttc ctgcgcacatcc 650  
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cagcgtgcgg tacctctgca tgggcgccga cggcaagatg caggggctgc 800  
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gaggtttggtt ttgtatatta aaatggagtt tgtttgt 2137  
  
<210> 86  
<211> 216  
<212> PRT  
<213> Homo Sapien  
  
<400> 86  
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Leu Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala  
20 25 30  
Gly Pro His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg  
35 40 45  
His Leu Tyr Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu  
50 55 60  
Arg Ile Arg Ala Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser  
65 70 75  
Ala His Ser Leu Leu Glu Ile Lys Ala Val Ala Leu Arg Thr Val  
80 85 90  
Ala Ile Lys Gly Val His Ser Val Arg Tyr Leu Cys Met Gly Ala  
95 100 105  
Asp Gly Lys Met Gln Gly Leu Leu Gln Tyr Ser Glu Glu Asp Cys  
110 115 120  
Ala Phe Glu Glu Glu Ile Arg Pro Asp Gly Tyr Asn Val Tyr Arg  
125 130 135  
Ser Glu Lys His Arg Leu Pro Val Ser Leu Ser Ser Ala Lys Gln  
140 145 150  
Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu Pro Leu Ser His Phe  
155 160 165  
Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro Glu Asp Leu Arg  
170 175 180  
Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu Glu Thr Asp  
185 190 195  
Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala Val Arg  
200 205 210  
Ser Pro Ser Phe Glu Lys  
215

<210> 87  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 87  
atccgcccag atggctacaa tgtgta 26

<210> 88  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 88  
gcctcccggt ctccctgagc agtgccaaac agccgcgtg ta 42

<210> 89  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 89  
ccagtccggc gacaagccca aa 22

<210> 90  
<211> 1857  
<212> DNA  
<213> Homo Sapien

<400> 90  
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aaaaaaaa 1857

<210> 91  
<211> 299

<212> PRT  
<213> Homo Sapien

<400> 91

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Val	His	Ser	Ser	Glu	Pro	Glu	Val	Arg	Ile	Pro	Glu	Asn	Asn	Pro
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Val	Lys	Leu	Ser	Cys	Ala	Tyr	Ser	Gly	Phe	Ser	Ser	Pro	Arg	Val
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Glu	Trp	Lys	Phe	Asp	Gln	Gly	Asp	Thr	Thr	Arg	Leu	Val	Cys	Tyr
	65						70					75		
Asn	Asn	Lys	Ile	Thr	Ala	Ser	Tyr	Glu	Asp	Arg	Val	Thr	Phe	Leu
	80					85					90			
Pro	Thr	Gly	Ile	Thr	Phe	Lys	Ser	Val	Thr	Arg	Glu	Asp	Thr	Gly
	95						100					105		
Thr	Tyr	Thr	Cys	Met	Val	Ser	Glu	Glu	Gly	Gly	Asn	Ser	Tyr	Gly
	110					115					120			
Glu	Val	Lys	Val	Lys	Leu	Ile	Val	Leu	Val	Pro	Pro	Ser	Lys	Pro
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Thr	Val	Asn	Ile	Pro	Ser	Ser	Ala	Thr	Ile	Gly	Asn	Arg	Ala	Val
	140					145					150			
Leu	Thr	Cys	Ser	Glu	Gln	Asp	Gly	Ser	Pro	Pro	Ser	Glu	Tyr	Thr
	155						160					165		
Trp	Phe	Lys	Asp	Gly	Ile	Val	Met	Pro	Thr	Asn	Pro	Lys	Ser	Thr
	170						175					180		
Arg	Ala	Phe	Ser	Asn	Ser	Ser	Tyr	Val	Leu	Asn	Pro	Thr	Thr	Gly
	185					190					195			
Glu	Leu	Val	Phe	Asp	Pro	Leu	Ser	Ala	Ser	Asp	Thr	Gly	Glu	Tyr
	200						205					210		
Ser	Cys	Glu	Ala	Arg	Asn	Gly	Tyr	Gly	Thr	Pro	Met	Thr	Ser	Asn
	215						220					225		
Ala	Val	Arg	Met	Glu	Ala	Val	Glu	Arg	Asn	Val	Gly	Val	Ile	Val
	230						235					240		
Ala	Ala	Val	Leu	Val	Thr	Leu	Ile	Leu	Leu	Gly	Ile	Leu	Val	Phe
	245						250					255		
Gly	Ile	Trp	Phe	Ala	Tyr	Ser	Arg	Gly	His	Phe	Asp	Arg	Thr	Lys
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<210> 92  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
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<210> 93  
<211> 50  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
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<210> 94  
<211> 20  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
acacctgggtt caaagatggg 20

<210> 95  
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<400> 95  
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<210> 96  
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<220>  
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<400> 96  
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<211> 1200  
<212> DNA  
<213> Homo Sapien  
  
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gtgagggacc agggcgccat gaccgaccag ctgagcaggc ggcagatccg 150  
cgagtaccaa ctctacagca ggaccagtgg caagcacgtg caggtcaccg 200  
ggcgtcgcat ctccgccacc gccgaggacg gcaacaagtt tgccaagctc 250  
atagtggaga cggacacgtt tggcagccgg gttcgcatca aaggggctga 300  
gagtgagaag tacatctgtt tgaacaagag gggcaagctc atcgggaagc 350  
ccagcgggaa gagcaaagac tgcgtgttca cggagatcgt gctggagaac 400  
aactatacgg cttccagaa cgcggcac gagggcttgtt tcatggcctt 450  
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 tcggatctcc ctcagtctgc ccccagcccc caaactcctc ctggctagac 1050  
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     20                  25                  30  
  
 Ala Met Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln  
     35                  40                  45  
  
 Leu Tyr Ser Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg  
     50                  55                  60  
  
 Arg Ile Ser Ala Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu  
     65                  70                  75  
  
 Ile Val Glu Thr Asp Thr Phe Gly Ser Arg Val Arg Ile Lys Gly  
     80                  85                  90  
  
 Ala Glu Ser Glu Lys Tyr Ile Cys Met Asn Lys Arg Gly Lys Leu  
     95                  100                 105  
  
 Ile Gly Lys Pro Ser Gly Lys Ser Lys Asp Cys Val Phe Thr Glu  
   110                  115                 120  
  
 Ile Val Leu Glu Asn Asn Tyr Thr Ala Phe Gln Asn Ala Arg His  
   125                  130                 135  
  
 Glu Gly Trp Phe Met Ala Phe Thr Arg Gln Gly Arg Pro Arg Gln  
   140                  145                 150  
  
 Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu Ala His Phe Ile Lys  
   155                  160                 165  
  
 Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn His Ala Glu Lys  
   170                  175                 180  
  
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 Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
   200                  205

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<211> 28  
<212> DNA  
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<400> 100  
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<210> 101  
<211> 24  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 101  
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<210> 102  
<211> 41  
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<212> DNA  
<213> Homo Sapien

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caaaaaagaa gaaaaagaag aagaaaaaaaaa atcatgaaaa ccatccagcc 150  
aaaaatgcac aattcttatct cttggcaat cttcacgggg ctggctgctc 200  
tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc cacctcccc 250  
aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300  
gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350

ccatccctcta tgctggaaat gacaagtggc gcctggatcc tcgcgtggc 400  
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aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 104  
<211> 344  
<212> PRT  
<213> Homo Sapien

<400> 104

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				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
				125					130					135	
Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
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Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	

Ser	Glu	His	Asp	Tyr	Gly	Asn	Tyr	Thr	Cys	Val	Ala	Ser	Asn	Lys
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Leu	Gly	His	Thr	Asn	Ala	Ser	Ile	Met	Leu	Phe	Gly	Pro	Gly	Ala
305							310					315		
Val	Ser	Glu	Val	Ser	Asn	Gly	Thr	Ser	Arg	Arg	Ala	Gly	Cys	Val
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Trp	Leu	Leu	Pro	Leu	Leu	Val	Leu	His	Leu	Leu	Leu	Lys	Phe	
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<210> 105  
 <211> 1734  
 <212> DNA  
 <213> Homo Sapien

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 agacactctg gagagagagg gggctggca gagatgaagt tccaggggcc 200  
 cctggcctgc ctccctgctgg ccctctgcct gggcagtggg gaggctggcc 250  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
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<210> 106  
 <211> 440  
 <212> PRT  
 <213> Homo Sapien

<400> 106  
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 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly  
 50 55 60  
 Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr  
 65 70 75  
 Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly  
 80 85 90  
 Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala  
 95 100 105  
 Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val

110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg	Gly Ser Trp Gln Gly Val	
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr	Ser Gly Gly His Gly Ile	
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly	Gln Gly Gln Gly Asn Pro	
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His	Gly Tyr Pro Gly Asn Ser	
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln	Gly Ala Pro Trp Gly Gln	
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe	Gly Thr Asn Thr Gln Gly	
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser	Val Arg Ala Ser Asn Gln	
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro	Ser Gly Ser Gly Gly Gly	
230	235	240
Ser Ser Asn Ser Gly Gly Ser Gly	Ser Gln Ser Gly Ser Ser	
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn	Asn Gly Ser Ser Ser Gly	
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly	Ser Ser Ser Gly Gly Ser	
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser	Gly Asn Ser Gly Gly Ser	
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser	Trp Gly Ser Ser Thr Gly	
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser	Gly Gly Asn Gly His	
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn	Glu Ala Arg Gly Ser Gly	
335	340	345
Glu Ser Gly Ile Gln Gly Phe Arg Gly	Gln Gly Val Ser Ser Asn	
350	355	360
Met Arg Glu Ile Ser Lys Glu Gly Asn	Arg Leu Leu Gly Gly Ser	
365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser	Ser Trp Gly Ser Gly Gly	
380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr	Val Asn Ser Glu Thr Ser	
395	400	405

Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
 410 415 420

Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg  
 425 430 435

Ser Ser Arg Ile Pro  
 440

<210> 107  
 <211> 918  
 <212> DNA  
 <213> Homo Sapien

<400> 107 .  
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 agcaatggca atgggggtcc ccagagtcat tctgctctgc ctctttgggg 100  
 ctgcgcctcg cctgacaggg tcccaagccc tgcagtgcta cagctttgag 150  
 cacacctact ttggccctt tgacctcagg gccatgaagc tgcccagcat 200  
 ctcctgtcct catgagtgct ttgaggctat cctgtctctg gacaccgggt 250  
 atcgcgccgccc ggtgaccctg gtgcggaaagg gctgctggac cgggcctcct 300  
 gcgggccaga cgcaatcgaa cccggacgcg ctgcccggcag actactcggt 350  
 ggtgcgcggc tgcacaactg acaaattgcaa cgcccacctc atgactcatg 400  
 acggccctccc caacctgagc caagcacccg acccgccgac gctcagcggc 450  
 gcccggatgt acgcctgtat cggggtccac cagatgact ggcgtatcgg 500  
 caggtcccgaa cgagtccagt gtcaccagga ccagaccggc tgcttccagg 550  
 gcagtgccag aatgacagtt ggcaatttct cagtcctgtt gtacatcaga 600  
 acctgccacc ggcctcctg caccaccgag ggcaccacca gcccctggac 650  
 agccatcgac ctccagggtc cctgctgtga ggggtacctc tgcaacagga 700  
 aatccatgac ccagcccttc accagtgttt cagccaccac ccctccccga 750  
 gcactacagg tcctggccct gtcctccca gtcctcctgc tgggtgggct 800  
 ctcagcatag accggccctc cagatgtt gggacagggc tcacacaccc 850  
 cattcttgct gttcagccc ctatcacata gtcactgga aaatgtatgtt 900  
 aaagtaagaa ttgcaaaa 918

<210> 108  
 <211> 251  
 <212> PRT  
 <213> Homo Sapien

<400> 108

Met Ala Met Gly Val Pro Arg Val Ile Leu Leu Cys Leu Phe Gly  
1 5 10 15

Ala Ala Leu Cys Leu Thr Gly Ser Gln Ala Leu Gln Cys Tyr Ser  
20 25 30

Phe Glu His Thr Tyr Phe Gly Pro Phe Asp Leu Arg Ala Met Lys  
35 40 45

Leu Pro Ser Ile Ser Cys Pro His Glu Cys Phe Glu Ala Ile Leu  
50 55 60

Ser Leu Asp Thr Gly Tyr Arg Ala Pro Val Thr Leu Val Arg Lys  
65 70 75

Gly Cys Trp Thr Gly Pro Pro Ala Gly Gln Thr Gln Ser Asn Pro  
80 85 90

Asp Ala Leu Pro Pro Asp Tyr Ser Val Val Arg Gly Cys Thr Thr  
95 100 105

Asp Lys Cys Asn Ala His Leu Met Thr His Asp Ala Leu Pro Asn  
110 115 120

Leu Ser Gln Ala Pro Asp Pro Pro Thr Leu Ser Gly Ala Glu Cys  
125 130 135

Tyr Ala Cys Ile Gly Val His Gln Asp Asp Cys Ala Ile Gly Arg  
140 145 150

Ser Arg Arg Val Gln Cys His Gln Asp Gln Thr Ala Cys Phe Gln  
155 160 165

Gly Ser Gly Arg Met Thr Val Gly Asn Phe Ser Val Pro Val Tyr  
170 175 180

Ile Arg Thr Cys His Arg Pro Ser Cys Thr Thr Glu Gly Thr Thr  
185 190 195

Ser Pro Trp Thr Ala Ile Asp Leu Gln Gly Ser Cys Cys Glu Gly  
200 205 210

Tyr Leu Cys Asn Arg Lys Ser Met Thr Gln Pro Phe Thr Ser Ala  
215 220 225

Ser Ala Thr Thr Pro Pro Arg Ala Leu Gln Val Leu Ala Leu Leu  
230 235 240

Leu Pro Val Leu Leu Val Gly Leu Ser Ala  
245 250

<210> 109

<211> 1813

<212> DNA

<213> Homo Sapien

<400> 109

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gactccgtcc cggccaggga gggccatgat ttccctcccg gggccccctgg 150  
tgaccaactt gctgcggttt ttgttccctgg ggctgagtgc cctcgccccc 200  
ccctcgccgg cccagctgca actgcacttg cccgccaacc gggtgcaggc 250  
ggtggaggga gggaaagtgg tgcttccagc gtggtacacc ttgcacgggg 300  
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aaacagaaaag aaaaggagga tcaggtgttg tcctacatca atggggtcac 400  
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tctccaaggga gtaagccgc tgtccaatac cagtgggatc ggcagcttcc 700  
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ccggaccctg ccctggccca agagctcaga cacaatctcc aagaatggga 1050  
ccctttctc tgtcacctcc gcacgagccc tccggccacc ccatggccct 1100  
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gtgcctgtga tggtgccctgc ccagagtcaa gctggctctc tggatgatg 1300  
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ctgaaattag ctactcacca agagtgaggg gcagagactt ccagtcactg 1600  
agtctccag gcccccttga tctgtacccc acccctatct aacaccaccc 1650  
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tttgtatgaa aaa 1813

<210> 110  
<211> 390  
<212> PRT  
<213> Homo Sapien

<400> 110  
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Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln  
20 25 30  
Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly  
35 40 45  
Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val  
50 55 60  
Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe  
65 70 75  
Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly  
80 85 90  
Val Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro  
95 100 105  
Ser Arg Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp  
110 115 120  
Ser Gly Pro Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly  
125 130 135  
Lys Ser Arg Gly His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu  
140 145 150  
Val Pro Pro Ala Pro Pro Ser Cys Arg Leu Gln Gly Val Pro His  
155 160 165  
Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser Pro Arg Ser Lys  
170 175 180

Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro	Ser	Phe	Gln
185									190					195
Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser	Leu	Ser
200								205						210
Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys	Lys
215								220						225
Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu
230								235						240
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val
245								250						255
Gly	Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu
260								265						270
Tyr	His	Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile
275								280						285
Lys	Glu	Asp	Ala	Ile	Ala	Pro	Arg	Thr	Leu	Pro	Trp	Pro	Lys	Ser
290								295						300
Ser	Asp	Thr	Ile	Ser	Lys	Asn	Gly	Thr	Leu	Ser	Ser	Val	Thr	Ser
305								310						315
Ala	Arg	Ala	Leu	Arg	Pro	Pro	His	Gly	Pro	Pro	Arg	Pro	Gly	Ala
320								325						330
Leu	Thr	Pro	Thr	Pro	Ser	Leu	Ser	Ser	Gln	Ala	Leu	Pro	Ser	Pro
335								340						345
Arg	Leu	Pro	Thr	Thr	Asp	Gly	Ala	His	Pro	Gln	Pro	Ile	Ser	Pro
350								355						360
Ile	Pro	Gly	Gly	Val	Ser	Ser	Ser	Gly	Leu	Ser	Arg	Met	Gly	Ala
365								370						375
Val	Pro	Val	Met	Val	Pro	Ala	Gln	Ser	Gln	Ala	Gly	Ser	Leu	Val
380								385						390

<210> 111  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 111  
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<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 112  
attgtgggcc ttgcagacat agac 24  
  
<210> 113  
<211> 50  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 113  
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<210> 114  
<211> 2479  
<212> DNA  
<213> Homo Sapien  
  
<400> 114  
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ttgcacatgg aggacagcag caaagaggc aacacaggct gataagacca 100  
gagacagcag ggagattatt ttaccatacg ccctcaggac gttccctcta 150  
gctggagttc tggacttcaa cagaacccca tccagtcatt ttgattttgc 200  
tgtttatattt ttttttcttt ttcttttcc caccacattt tattttatattt 250  
ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300  
ctttttcctt gaagtcttgg cttatcattt ccctggggct ctactcacag 350  
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ttctccattt gcagaaaaac aatattcaga ccatttcacg ggctgctctt 650  
gcccagctct tgaagcttga agagctgcac ctggatgaca actccatatac 700  
cacagtgggg gtgaaagacg gggccttccg ggaggctatt agcctcaaatt 750  
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gagcagacga cgtcccacag catgggctcc ccctttctgc tggcgggctt 1900  
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<210> 115  
 <211> 660  
 <212> PRT  
 <213> Homo Sapien

<400> 115  
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 20 25 30

Ser Lys Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn  
 35 40 45

Phe Val Tyr Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly  
 50 55 60

Ile Pro Glu Gly Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile  
 65 70 75

Asn Asn Ala Gly Phe Pro Ala Glu Leu His Asn Val Gln Ser Val  
 80 85 90

His Thr Val Tyr Leu Tyr Gly Asn Gln Leu Asp Glu Phe Pro Met  
 95 100 105

Asn Leu Pro Lys Asn Val Arg Val Leu His Leu Gln Glu Asn Asn  
 110 115 120

Ile Gln Thr Ile Ser Arg Ala Ala Leu Ala Gln Leu Leu Lys Leu  
 125 130 135

Glu Glu Leu His Leu Asp Asp Asn Ser Ile Ser Thr Val Gly Val  
 140 145 150

Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser Leu Lys Leu Leu Phe  
 155 160 165

Leu Ser Lys Asn His Leu Ser Ser Val Pro Val Gly Leu Pro Val  
 170 175 180

Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile Ala Val Ile  
 185 190 195

Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg Leu Ile  
 200 205 210

Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly Thr  
 215 220 225

Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn

230	235	240
Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile		
245	250	255
Arg Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr		
260	265	270
Ala Phe Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn		
275	280	285
Asn Gln Leu Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser		
290	295	300
Asn Leu Lys Gln Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp		
305	310	315
Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser		
320	325	330
Ser Leu Asn Val Arg Gly Phe Met Cys Gln Gly Pro Glu Gln Val		
335	340	345
Arg Gly Met Ala Val Arg Glu Leu Asn Met Asn Leu Leu Ser Cys		
350	355	360
Pro Thr Thr Thr Pro Gly Leu Pro Leu Phe Thr Pro Ala Pro Ser		
365	370	375
Thr Ala Ser Pro Thr Thr Gln Pro Pro Thr Leu Ser Ile Pro Asn		
380	385	390
Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro Thr Thr Ser Lys Leu		
395	400	405
Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg Val Thr Pro Pro		
410	415	420
Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val Asn Asp Thr		
425	430	435
Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met Ala Tyr		
440	445	450
Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly Ile		
455	460	465
Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu		
470	475	480
Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro		
485	490	495
Leu Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser		
500	505	510
Glu Ala Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr		
515	520	525

Ala Ser Ser His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro  
530 535 540  
Phe Leu Leu Ala Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu  
545 550 555  
Val Val Leu Leu Ser Val Phe Cys Trp His Met His Lys Lys Gly  
560 565 570  
Arg Tyr Thr Ser Gln Lys Trp Lys Tyr Asn Arg Gly Arg Arg Lys  
575 580 585  
Asp Asp Tyr Cys Glu Ala Gly Thr Lys Lys Asp Asn Ser Ile Leu  
590 595 600  
Glu Met Thr Glu Thr Ser Phe Gln Ile Val Ser Leu Asn Asn Asp  
605 610 615  
Gln Leu Leu Lys Gly Asp Phe Arg Leu Gln Pro Ile Tyr Thr Pro  
620 625 630  
Asn Gly Gly Ile Asn Tyr Thr Asp Cys His Ile Pro Asn Asn Met  
635 640 645  
Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu His Cys His Thr  
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<210> 116

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

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<210> 117

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 117

gcaggacaac cagataaacc ac 22

<210> 118

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 118

acgcagattt gagaaggctg tc 22  
<210> 119  
<211> 46  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Synthetic oligonucleotide probe  
  
<400> 119  
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<210> 120  
<211> 2857  
<212> DNA  
<213> Homo Sapien  
  
<400> 120  
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caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150  
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cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550  
caagtgtatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
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cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700  
taatcattca agccaaaggac atgattggtc agccaggagc gttgtctgga 750  
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gcagaaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950  
tattactaat catgaaaactc aagaaggaat agttatatta aaaaagaaaag 1000

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gtaggcgtgg tgtctgccac agacccagac aataggaaat ctcctatcag 1250  
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tcactacaag taactcactg gatcgtgaaa tcagtgcctt gtaaaccta 1350  
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cagactatca gtgcagtggaa tagagatgaa tccatagaag agcaccattt 1550  
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tagataatca agataaacaca gctgtcattt tgactaatag aactggttt 1650  
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tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050  
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 <212> PRT  
 <213> Homo Sapien

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Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp
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Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser
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His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn
65								70					75	

Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe
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Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu
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Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile
110								115					120	

Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val
125								130					135	

Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp
140								145					150	

Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr
155								160					165	

Leu Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Ser Ser

170	175	180
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185	190	195
Tyr Phe Ser Val Glu Pro Thr Thr Gly	Val Ile Arg Ile Ser Ser	
200	205	210
Lys Met Asp Arg Glu Leu Gln Asp Glu	Tyr Trp Val Ile Ile Gln	
215	220	225
Ala Lys Asp Met Ile Gly Gln Pro Gly	Ala Leu Ser Gly Thr Thr	
230	235	240
Ser Val Leu Ile Lys Leu Ser Asp Val	Asn Asp Asn Lys Pro Ile	
245	250	255
Phe Lys Glu Ser Leu Tyr Arg Leu Thr	Val Ser Glu Ser Ala Pro	
260	265	270
Thr Gly Thr Ser Ile Gly Thr Ile Met	Ala Tyr Asp Asn Asp Ile	
275	280	285
Gly Glu Asn Ala Glu Met Asp Tyr Ser	Ile Glu Glu Asp Asp Ser	
290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His	Glu Thr Gln Glu Gly Ile	
305	310	315
Val Ile Leu Lys Lys Val Asp Phe	Glu His Gln Asn His Tyr	
320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His	His Val Pro Glu Gln Leu	
335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr	Thr Phe Ile Lys Ile Gln	
350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr Tyr	
365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val Gly	
380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile Arg	
395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn Gly	
410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala Trp	
425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu Gln	
440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn Asp	
455	460	465

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515														525
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu
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Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala
590														600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr
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620														630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly
635														645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg
650														660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser
665														675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro
680														690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu
695														705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr
710														720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser
725														735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu
740														750
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755

760

765

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gcagctgcgc ccatcagctc ccactgcagg ctt  
  
gcagccctat atcaccaacc gcacccat gct  
  
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<213> Homo Sapien

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Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser  
35 40 45  
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50 55 60  
Lys Glu Ala Ser Leu Ala Asp Asn Thr Asp Val Arg Leu Ile  
65 70 75  
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr

80	85	90
Leu Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe		
95	100	105
Pro Gln Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro		
110	115	120
Phe Leu Ala Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu		
125	130	135
Gly Asp Asp Leu His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp		
140	145	150
Thr Val Lys Lys Leu Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly		
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Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn Ala Cys Ile		
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<212> DNA
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 <212> PRT  
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Lys Pro Gly Asp Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln  
 35 40 45

Ala Phe Pro His Thr Glu Glu Glu Val Glu Val Asp Ser His Ala  
 50 55 60

Tyr Ser His Arg Trp Lys Arg Asn Leu Asp Phe Leu Lys Ala Val  
 65 70 75

Asp Thr Asn Arg Ala Ser Val Gly Gln Asp Ser Pro Glu Pro Arg  
 80 85 90

Ser Phe Thr Asp Leu Leu Leu Asp Asp Gly Gln Asp Asn Asn Thr  
 95 100 105

Gln Ile Glu Glu Asp Thr Asp His Asn Tyr Tyr Ile Ser Arg Ile  
 110 115 120

Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp Leu Trp Val Asn Ile  
 125 130 135

Asp Gln Met Glu Lys Asp Lys Val Lys Ile His Gly Ile Leu Ser  
 140 145 150

Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser Phe Asp Phe  
 155 160 165

Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala Thr Gly  
 170 175 180

Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr Ala  
 185 190 195

Thr	Gln	Tyr	Ile	Ala	Pro	Leu	Met	Ala	Asn	Phe	Asp	Pro	Ser	Val
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Ser	Arg	Asn	Ser	Thr	Val	Arg	Tyr	Phe	Asp	Asn	Gly	Thr	Ala	Leu
215								220						225
Val	Val	Gln	Trp	Asp	His	Val	His	Leu	Gln	Asp	Asn	Tyr	Asn	Leu
230								235						240
Gly	Ser	Phe	Thr	Phe	Gln	Ala	Thr	Leu	Leu	Met	Asp	Gly	Arg	Ile
245								250						255
Ile	Phe	Gly	Tyr	Lys	Glu	Ile	Pro	Val	Leu	Val	Thr	Gln	Ile	Ser
260								265						270
Ser	Thr	Asn	His	Pro	Val	Lys	Val	Gly	Leu	Ser	Asp	Ala	Phe	Val
275								280						285
Val	Val	His	Arg	Ile	Gln	Gln	Ile	Pro	Asn	Val	Arg	Arg	Arg	Thr
290								295						300
Ile	Tyr	Glu	Tyr	His	Arg	Val	Glu	Leu	Gln	Met	Ser	Lys	Ile	Thr
305								310						315
Asn	Ile	Ser	Ala	Val	Glu	Met	Thr	Pro	Leu	Pro	Thr	Cys	Leu	Gln
320								325						330
Phe	Asn	Arg	Cys	Gly	Pro	Cys	Val	Ser	Ser	Gln	Ile	Gly	Phe	Asn
335								340						345
Cys	Ser	Trp	Cys	Ser	Lys	Leu	Gln	Arg	Cys	Ser	Ser	Gly	Phe	Asp
350								355						360
Arg	His	Arg	Gln	Asp	Trp	Val	Asp	Ser	Gly	Cys	Pro	Glu	Glu	Ser
365								370						375
Lys	Glu	Lys	Met	Cys	Glu	Asn	Thr	Glu	Pro	Val	Glu	Thr	Ser	Ser
380								385						390
Arg	Thr	Thr	Thr	Thr	Val	Gly	Ala	Thr	Thr	Thr	Gln	Phe	Arg	Val
395								400						405
Leu	Thr	Thr	Thr	Arg	Arg	Ala	Val	Thr	Ser	Gln	Phe	Pro	Thr	Ser
410								415						420
Leu	Pro	Thr	Glu	Asp	Asp	Thr	Lys	Ile	Ala	Leu	His	Leu	Lys	Asp
425								430						435
Asn	Gly	Ala	Ser	Thr	Asp	Asp	Ser	Ala	Ala	Glu	Lys	Lys	Gly	Gly
440								445						450
Thr	Leu	His	Ala	Gly	Leu	Ile	Ile	Gly	Ile	Leu	Ile	Leu	Val	Leu
455								460						465
Ile	Val	Ala	Thr	Ala	Ile	Leu	Val	Thr	Val	Tyr	Met	Tyr	His	His
470								475						480
Pro	Thr	Ser	Ala	Ala	Ser	Ile	Phe	Phe	Ile	Glu	Arg	Arg	Pro	Ser

485 490 495  
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515 520 525  
Ser Glu Gln Cys

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<212> DNA  
<213> Homo Sapien

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<223> unknown base

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cctcctgcct cccggctgga cagagtgtgg acttcccctg ggcggccgtg 150  
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tgatgagaga caatttaata acagtatagt aaatatacca tatgatttct 1950  
ttagttgtag ctaaatgtta gatccaccgt gggaaatcat tccctttaaa 2000  
atgacagcac agtccactca aaggattgcc tagcaataca gcatctttc 2050  
ctttcactag tccaagccaa aaattttaag atgattgtc agaaaggcga 2100  
caaagtccata tcacctaata ttacaagagt tggttaagcgc tcatttcata 2150  
ttttattttg tggcagctaa gttagttatga cagaggcagt gtcctgtgg 2200  
acaggagcat tttgcattt ttccatctga aagtatcact cagttgatag 2250  
tctggaatgc atgttatata tttaaaact tccaaaatatt attataacaa 2300  
acattctata tcggatgtta gcagaccaat ctctaaaata gctaattctt 2350

caataaaatc tttctatata gccatttcag tgcaaacaag taaaatcaa 2400  
aaagaccatc ctttattttt ctttacatga tataatgtaa atgcgatcaa 2450  
ataaaagacaa aacaccagtg atgagaatat cttaagataa gtaattatca 2500  
aattattgtg aatgttaaat tatttctact ataaagaagc aaaactacat 2550  
ttttgaagga aaatgtgtt actctaacat taatttacag gaatagttt 2600  
atggtttac tctttactaa agaaaggcca tcaccttcaa agccatttt 2650  
caggtttgcat gaagttacca atttcagttt acctaaatctt ctacaaatag 2700  
tcccccttta caagttgtaa caacaaagac cctataataa aatttagatac 2750  
aagaaatttt gcagtggta tacatatttgc agatatctt tagttgccc 2800  
tagcagggat ggcttaaaaaa ctgtgatttt ttttcttcaa gtaaaactta 2850  
gtcccaaagt acatcataaa tcaattttaa ttagaaaaat gaatcttaaa 2900  
tgaggggaca taagtataact ctttccacaa aatggcaata ataaggcata 2950  
aagctagtaa atctactaac tgtaataat gtatgacatt attttgcattt 3000  
atacattaaa aaagagtttt tagaacaaat atggcattta actttattat 3050  
ttatggctt ttaagaaata ttctttgtgg aattgttcaa taaactataa 3100  
aatattattt tgtattgcag cttttaaagtgc gcacactcca taataatcta 3150  
cttactagaa atagtggtgc taccacaaaa aatgttaacc atcagtacca 3200  
ttgtttggga gaaagaaaca gatcaagaat gcatattattt cagtgaccgc 3250  
tttccttagag ttaaaatacc tcctcttgc aaggttgtt ggtaaattgtt 3300  
ggtataaaact atggatgaac caaataatgtt gttcaaaatgtt ttgtcatgtt 3350  
tccaaatttgc tggagtctgg tggttttacc atagaatgtt acagaagttt 3400  
agtcatagct cagtagctat atgtatttgc ctttatgtt gaagagactt 3450  
tcttgagtgtt cattttaaa tagaggaggtt attcaatgtt ttttctgtt 3500  
tcacagcagc attccttagtc ctttaggcctt cggacagagt gaaatcatgtt 3550  
gtatattatgtt gttcaatattt gtcaaaataag gctacagtat ttgtttttttt 3600  
gtgtgaatgtt attgcataatgtt atgttcaagt agatgattttt acatttatgg 3650  
acatataaaa tgtctgatta ccccatatgtt tcagtcctgtt ctgtacaaga 3700  
ttgttgcaat ttcaaaatgtt cagttttata aattgttcaatgtt tcttttaatc 3750  
tataacaattt tgtgttagct gttcatttca ggantatattt ttctacaatgtt 3800

tccacttgc ggactccctt tggccctt atttttttt aaagaaggaa 3850  
gaaagaaaaa taatggcag tttaaaaatg agaatggaga gaaaagaaaa 3900  
agaatgaaaa ggaaaggcag taaagaggaa aaaaaaagga aggatgaaag 3950  
gaatgaagga aggaagggag gaaggggaga aggttaggaag aaagaaagga 4000  
tgagagggaa ggaagaatca gagtattag gtatgttact tacacattt 4050  
cattcttagt ttaactgcaa gtgggtgttac tatgttttc aatgatcgca 4100  
tttggaaacat aagtccattt ataccattaa gttccttattt tgcagcaatt 4150  
atataataaa aagtactgcc caagttatag taatgtgggt gttttgaga 4200  
caactaaaaga tttgagaggg agaatttcaa acttaaagcc acttttgggg 4250  
ggtttataaac ttaactgaaa aattaatgct tcatacataac atttaagcta 4300  
tatctagaaaa gtagactgga gaaactgagaa aattaccag gtaattcagg 4350  
gaaaaaaaaa aatatatata tatataaata cccctacatt tgaagtcaga 4400  
aaactctgaa aaactgaatt atcaaagtca atcatctata atgatcaaat 4450  
ttactgaaca attgttattt tatccattgt gcttagctt gtgacacagc 4500  
caaaagttac ctatataatc tttcaataa aaattgtttt ttgaaatcca 4550  
gaaatgattt aaaaagaggt cagggtttt actattttt gaagtatgtg 4600  
gatgtacagt atttcaatag atatgaatat gaataaatgg tatgccttaa 4650  
gattcttga atatgtatTTT actttaaaga ctggaaaaag ctcttcctgt 4700  
cttttagtaa aacatccata tttcataacc tgatgtaaaa tatgttgcac 4750  
tgtttccat aggtgaatat aaactcagtt tatcaattaa aaaaaaaaaa 4800  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 4834

<210> 130  
<211> 354  
<212> PRT  
<213> Homo Sapien

<400> 130  
Met Asp Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln  
1 5 10 15  
Trp Leu Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser  
20 25 30  
Cys Leu Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val  
35 40 45  
Asp Asn Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys

50	55	60
Tyr Leu Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser		
65	70	75
Ser Ile Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg		
80	85	90
Val Ser Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile		
95	100	105
Gln Asn Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val		
110	115	120
Gln Thr Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val		
125	130	135
Gln Val Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val		
140	145	150
Asn Glu Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys		
155	160	165
Pro Glu Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys		
170	175	180
Pro Phe Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg		
185	190	195
Asp Gln Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Asp Val Ser		
200	205	210
Phe Pro Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro		
215	220	225
Thr Ile Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser		
230	235	240
Gly Leu Ile Arg Cys Glu Gly Ala Gly Val Pro Pro Pro Ala Phe		
245	250	255
Glu Trp Tyr Lys Gly Glu Lys Lys Leu Phe Asn Gly Gln Gln Gly		
260	265	270
Ile Ile Ile Gln Asn Phe Ser Thr Arg Ser Ile Leu Thr Val Thr		
275	280	285
Asn Val Thr Gln Glu His Phe Gly Asn Tyr Thr Cys Val Ala Ala		
290	295	300
Asn Lys Leu Gly Thr Thr Asn Ala Ser Leu Pro Leu Asn Pro Pro		
305	310	315
Ser Thr Ala Gln Tyr Gly Ile Thr Gly Ser Ala Asp Val Leu Phe		
320	325	330
Ser Cys Trp Tyr Leu Val Leu Thr Leu Ser Ser Phe Thr Ser Ile		
335	340	345

Phe Tyr Leu Lys Asn Ala Ile Leu Gln  
350

<210> 131  
<211> 823  
<212> DNA  
<213> Homo Sapien

<400> 131  
atagtagaag aatgtctctg aaattactgg atgagtttca gtcataacttt 50  
cacatggcca caatttcaca ttcaagctcc ttatcctagg ctaattttat 100  
attatgttaa atcacttgtt tttgttctca cggcttcctg cctgctatag 150  
gcataattac gaggaagcag aacttctcca gaagcaagcg cacatgcgtt 200  
ccaaaataag agcaaattcg ctctaaacac agaaaaagac ctgaagcttt 250  
aattaagggg ttacatccaa ccccagagcg cttttgtggg cactgattgc 300  
tccagcttct gcgtcactgc gcgagggaaag agggaaagagg atccaggcgt 350  
tagacatgta tagacacaaa aacagctgga gattggcctt aaaataccca 400  
ccaagctcca aagaagagac ccaagtcccc aaaacattga tttcagggct 450  
gccaggaagg aagagcagca gcaggggtggg agagaagctc cagtcagccc 500  
acaagatgcc attgtcccc ggcctctgc tgctgctgct ctccggggcc 550  
acggccacccg ctgcctgccc cctggagggt ggccccacccg gccgagacag 600  
cgagcatatg caggaagcgg caggaataag gaaaagcagc ctccctgactt 650  
tcctcgcttg gtggtttgag tggacctccc aggccagtgc cgggccccctc 700  
ataggagagg aagctcgaaa ggtggccagg cggcaggaag ggcacccccc 750  
ccagcaatcc gcgccccggg acagaatgcc ctgcaggaac ttcttctgga 800  
agaccttctc ctccatccaa tag 823

<210> 132  
<211> 155  
<212> PRT  
<213> Homo Sapien

<400> 132  
Met Tyr Arg His Lys Asn Ser Trp Arg Leu Gly Leu Lys Tyr Pro  
1 5 10 15  
Pro Ser Ser Lys Glu Glu Thr Gln Val Pro Lys Thr Leu Ile Ser  
20 25 30  
Gly Leu Pro Gly Arg Lys Ser Ser Ser Arg Val Gly Glu Lys Leu  
35 40 45

Gln Ser Ala His Lys Met Pro Leu Ser Pro Gly Leu Leu Leu Leu  
50 55 60

Leu Leu Ser Gly Ala Thr Ala Thr Ala Ala Leu Pro Leu Glu Gly  
65 70 75

Gly Pro Thr Gly Arg Asp Ser Glu His Met Gln Glu Ala Ala Gly  
80 85 90

Ile Arg Lys Ser Ser Leu Leu Thr Phe Leu Ala Trp Trp Phe Glu  
95 100 105

Trp Thr Ser Gln Ala Ser Ala Gly Pro Leu Ile Gly Glu Glu Ala  
110 115 120

Arg Glu Val Ala Arg Arg Gln Glu Gly Ala Pro Pro Gln Gln Ser  
125 130 135

Ala Arg Arg Asp Arg Met Pro Cys Arg Asn Phe Phe Trp Lys Thr  
140 145 150

Phe Ser Ser Cys Lys  
155

<210> 133  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 133  
tcagggtctgc caggaaggaa gagc 24

<210> 134  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 134  
gcaggaggag aaggcttcc agaagaag 28

<210> 135  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 135  
agaagttcca gtcagccac aagatgccat tgtccccgg cctcc 45

<210> 136

<211> 1875  
<212> DNA  
<213> Homo Sapien

<400> 136  
gtcgtgtgct tggaggaagc cgcgaaaccc ccagcgtccg tccatggcgt 50  
ggagccttgg gagctggctg ggtggctgcc tgctgggtgc agcattggga 100  
atggtaccac ctcccgaaaaa tgcagaatg aattctgtta atttcaagaa 150  
cattctacag tgggagtcac ctgccttgc caaaggaaac ctgactttca 200  
cagctcagta cctaaagttat aggatattcc aagataaattg catgaatact 250  
accttgacgg aatgtgattt ctcaagtctt tccaaagtatg gtgaccacac 300  
cttgagagtc agggctgaat ttgcagatga gcattcagac tgggtaaaca 350  
tcacccctcg tcctgtggat gacaccatta ttggacccccc tggaaatgcaa 400  
gtagaagtac ttgcgtattc ttacatatg cgtttcttag cccctaaaaat 450  
tgagaatgaa tacgaaactt ggactatgaa gaatgtgtat aactcatgga 500  
cttataatgt gcaatactgg aaaaacgta ctgatgaaaaa gtttcaaatt 550  
actccccagt atgactttga ggtcctcaga aacctggagc catggacaac 600  
ttattgtgtt caagttcgag ggttcttcc tgatcggAAC aaagctgggg 650  
aatggagtga gcctgtctgt gagcaaacaa cccatgacga aacggcccc 700  
tcctggatgg tggccgtcat cctcatgcc tcggcttca tggctgcct 750  
ggcactcctc ggctgcttct ctttgctgtg gtgcgtttac aagaagacaa 800  
agtacgcctt ctcccttagg aattctcttc cacagcacct gaaagagttt 850  
ttgggccatc ctcataa cacacttctg ttttcttcc ttccattgtc 900  
ggatgagaat gatgttttg acaagctaag tgtcattgca gaagactctg 950  
agagcggcaa gcagaatcct ggtgacagct gcagcctcgg gacccgcct 1000  
gggcaggggc cccaaagcta ggctctgaga agggaaacaca ctggctggg 1050  
cacagtgacg tactccatct cacatctgcc tcagtgaggg atcaggcag 1100  
caaacaaggc ccaagaccat ctgagccagc cccacatcta gaactccaga 1150  
cctggactta gccaccagag agtacatatt taaaggctgt ctggcaaaa 1200  
atactccatt tggaaactca ctgccttata aaggcttca tgatgtttc 1250  
agaagttggc cactgagagt gtaatttca gcctttata tcactaaaaat 1300  
aagatcatgt tttaattgtg agaaacaggg ccgagcacag tggctcacgc 1350

ctgtaatacc agcaccttag aggtcgaggc aggccgatca cttgagggtca 1400  
ggagttcaag accagcctgg ccaatatggt gaaacccagt ctctactaaa 1450  
aatacaaaaa ttagcttaggc atgatggcgc atgcctataa tcccagctac 1500  
tcgagtcct gaggcaggag aattgcatga acccgggagg aggaggagga 1550  
ggttgcagtg agccgagata gcggcactgc actccagcct gggtgacaaa 1600  
gtgagactcc atctcaaaaa aaaaaaaaaa aaattgttag aaacagaaaat 1650  
acttaaaatg aggaataaga atggagatgt tacatctggt agatgtaaaca 1700  
ttctaccaga ttatggatgg actgatctga aaatcgacct caactcaagg 1750  
gtggtcagct caatgtaca cagagcacgg acttttgat tctttgcagt 1800  
actttgaatt tattttcta cctatataatg ttttatatgc tgctggtgct 1850  
ccattaaagt tttactctgt gttgc 1875

<210> 137  
<211> 325  
<212> PRT  
<213> Homo Sapien

<400> 137  
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val  
1 5 10 15  
Ser Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn  
20 25 30  
Ser Val Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe  
35 40 45  
Ala Lys Gly Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg  
50 55 60  
Ile Phe Gln Asp Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp  
65 70 75  
Phe Ser Ser Leu Ser Lys Tyr Gly Asp His Thr Leu Arg Val Arg  
80 85 90  
Ala Glu Phe Ala Asp Glu His Ser Asp Trp Val Asn Ile Thr Phe  
95 100 105  
Cys Pro Val Asp Asp Thr Ile Ile Gly Pro Pro Gly Met Gln Val  
110 115 120  
Glu Val Leu Ala Asp Ser Leu His Met Arg Phe Leu Ala Pro Lys  
125 130 135  
Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn Val Tyr Asn  
140 145 150

Ser	Trp	Thr	Tyr	Asn	Val	Gln	Tyr	Trp	Lys	Asn	Gly	Thr	Asp	Glu
155									160					165
Lys	Phe	Gln	Ile	Thr	Pro	Gln	Tyr	Asp	Phe	Glu	Val	Leu	Arg	Asn
170									175					180
Leu	Glu	Pro	Trp	Thr	Thr	Tyr	Cys	Val	Gln	Val	Arg	Gly	Phe	Leu
185									190					195
Pro	Asp	Arg	Asn	Lys	Ala	Gly	Glu	Trp	Ser	Glu	Pro	Val	Cys	Glu
200									205					210
Gln	Thr	Thr	His	Asp	Glu	Thr	Val	Pro	Ser	Trp	Met	Val	Ala	Val
215									220					225
Ile	Leu	Met	Ala	Ser	Val	Phe	Met	Val	Cys	Leu	Ala	Leu	Leu	Gly
230									235					240
Cys	Phe	Ser	Leu	Leu	Trp	Cys	Val	Tyr	Lys	Lys	Thr	Lys	Tyr	Ala
245									250					255
Phe	Ser	Pro	Arg	Asn	Ser	Leu	Pro	Gln	His	Leu	Lys	Glu	Phe	Leu
260									265					270
Gly	His	Pro	His	His	Asn	Thr	Leu	Leu	Phe	Phe	Ser	Phe	Pro	Leu
275									280					285
Ser	Asp	Glu	Asn	Asp	Val	Phe	Asp	Lys	Leu	Ser	Val	Ile	Ala	Glu
290									295					300
Asp	Ser	Glu	Ser	Gly	Lys	Gln	Asn	Pro	Gly	Asp	Ser	Cys	Ser	Leu
305									310					315
Gly	Thr	Pro	Pro	Gly	Gln	Gly	Pro	Gln	Ser					
320									325					

<210> 138  
 <211> 2570  
 <212> DNA  
 <213> Homo Sapien

<400> 138  
 cgagcgccaa cccgctagcg cctgaatccg gctgtctgcc cgctcgccgc 50  
 ccggccatggc ccgcgcagcc ccgctgctcg ccgcgttgac cgcgctccctc 100  
 gccgcgcgcg ctgctggcgg agatccccg ccggggaaaa tcgcgggtgg 150  
 tggggctggg attggggct ctgctgtggc ccattttctc cagcagcact 200  
 ttggacctcg ggtgcagatc gacgtgtacg agaaggaaac cgtgggtggc 250  
 cgcttggcca ccatctcagt caacaaggcag cactatgaga gcggggctgc 300  
 ctccctccac tccctgagcc tgcacatgca ggacttcgtc aagctgctgg 350  
 ggctgaggca cggcgccgag gtggtggca ggagcgccat cttcgccgg 400

gagcacttca tgctggagga gactgactgg tacctgctga acctcttccg 450  
cctctggtgg cactatggca tcagcttccct gaggctgcag atgtgggtgg 500  
aggaggtcat ggagaagttc atgaggatct ataagtacca ggcccacggc 550  
tatgccttct cgggtgtgga ggagctgctc tactcaactgg gggagtccac 600  
ctttgttaac atgacccagc actctgtggc tgagtccctg ctgcagggtgg 650  
gcgtcacgca gcgcatttatt gatgatgtcg ttctgtgt cctgcgggcc 700  
agctatggcc agtcagcagc gatgcccggc tttgcaggag ccatgtcact 750  
agccggggcc caaggcagcc tgtggtctgt ggaaggaggc aataagctgg 800  
tttgttccgg tttgtgaag ctcaccaagg ccaatgtgat ccatgccaca 850  
tgacaccttg tgaccctgca cagcacagag gggaaagccc tgtaccaggt 900  
ggcgtatgag aatgaggttag gcaacagctc tgacttctat gacatcgtgg 950  
tcatgccac cccctgcac ctggacaaca gcagcagcaa cttAACCTT 1000  
gcaggcttcc acccgcccat tgatgacgtg cagggttctt tccagccac 1050  
cgtcgtctcc ttggccacg gctacctcaa ctgcgtctac ttgggttcc 1100  
cagaccctaa gctttcccc tttgccaaca tccttaccac agatttcccc 1150  
agcttcttct gcactctgga caacatctgc cctgtcaaca tctctgccag 1200  
cttccggcga aagcagcccc aggaggcagc tgtttggcga gtccagtccc 1250  
ccaagccctt ctccggacc cagctaaaga ccctgttccg ttccattac 1300  
tcagtgaga cagctgagtg gcaggccat cccctctatg gtcggccccc 1350  
cacgctcccg aggtttgcac tccatgacca gctttctac ctcaatgccc 1400  
tggagtggc ggccagctcc gtggaggtga tggccgtggc tgccaagaat 1450  
gtggccttgc tggcttacaa ccgctggtag caggacctag acaagattga 1500  
tcaaaaagat ttgatgcaca aggtcaagac tgaactgtga gggctctagg 1550  
gagagcctgg gaactttcat cccccactga agatggatca tcccacagca 1600  
gcccaggact gaataagcca tgctcgccca ccaggcttct ttctgacccc 1650  
tcatgtatca agcatctcca ggtgacctac tgtctgccta tattaagggt 1700  
ccacacggcg gctgctgctt ttttttaagg gggaaagtaa gaaaagagaa 1750  
gaaaatccaa gccagtatat ttgttttatt tattttttt aagaagaaaa 1800  
aagttcatct tcacaagggtg ctccagactt ggtttcttag ctagaaacca 1850

gaagactacg ggagggaata taaggcagag aactatgagt cttattttat 1900  
tactgtttt cactacctac tcccacaatg gacaatcaat tgaggcaacc 1950  
tacaagaaaa catttacaac cagatggta caaataaaagt agaagggaaag 2000  
atcagaaaaac ctaagaaaatg atcatagctc ctggttactg tggacttgat 2050  
ggatttgaag tacctagttc agaactccct agtcaccatc tccaagcctg 2100  
tcaacatcac tgcataattgg aggagatgac tgtggtagga cccaaggaag 2150  
agatgtgtgc ctgaatagtc gtcaccatat ctccaagcctt cctggcaacc 2200  
agtggaaaaa gaaacatgcg aggctgtagg aagagggaaag ctcttccttg 2250  
gcacctagag gaattagcca ttctcttcct tatgcaaaga ttgaggaatg 2300  
caacaatata aagaagagaa gtccccagat ggtagagagc agtcataatct 2350  
tacccctaga tgttcatccc agcagaagaa agaagaaggt gttgggttag 2400  
gattcttcag aggttagcct ggtactttct catcagacac tagcttgaag 2450  
taagaggaga attatgcttt tctttgcttt ttctacaaac ccttaaaaat 2500  
cacttgtttt aaaaagaaag taaaagccct tttcattcaa aaaaaaaaaa 2550  
aaaaaaaaaaa aaaaaaaaaa 2570

<210> 139  
<211> 494  
<212> PRT  
<213> Homo Sapien

<400> 139  
Met Ala Arg Ala Ala Pro Leu Leu Ala Ala Leu Thr Ala Leu Leu  
1 5 10 15  
Ala Ala Ala Ala Gly Gly Asp Ala Pro Pro Gly Lys Ile Ala  
20 25 30  
Val Val Gly Ala Gly Ile Gly Gly Ser Ala Val Ala His Phe Leu  
35 40 45  
Gln Gln His Phe Gly Pro Arg Val Gln Ile Asp Val Tyr Glu Lys  
50 55 60  
Gly Thr Val Gly Gly Arg Leu Ala Thr Ile Ser Val Asn Lys Gln  
65 70 75  
His Tyr Glu Ser Gly Ala Ala Ser Phe His Ser Leu Ser Leu His  
80 85 90  
Met Gln Asp Phe Val Lys Leu Leu Gly Leu Arg His Arg Arg Glu  
95 100 105  
Val Val Gly Arg Ser Ala Ile Phe Gly Gly Glu His Phe Met Leu

110	115	120
Glu Glu Thr Asp Trp Tyr Leu Leu Asn	Leu Phe Arg Leu Trp Trp	
125	130	135
His Tyr Gly Ile Ser Phe Leu Arg Leu	Gln Met Trp Val Glu Glu	
140	145	150
Val Met Glu Lys Phe Met Arg Ile Tyr	Lys Tyr Gln Ala His Gly	
155	160	165
Tyr Ala Phe Ser Gly Val Glu Glu	Leu Leu Tyr Ser Leu Gly Glu	
170	175	180
Ser Thr Phe Val Asn Met Thr Gln His	Ser Val Ala Glu Ser Leu	
185	190	195
Leu Gln Val Gly Val Thr Gln Arg Phe	Ile Asp Asp Val Val Ser	
200	205	210
Ala Val Leu Arg Ala Ser Tyr Gly Gln	Ser Ala Ala Met Pro Ala	
215	220	225
Phe Ala Gly Ala Met Ser Leu Ala Gly	Ala Gln Gly Ser Leu Trp	
230	235	240
Ser Val Glu Gly Gly Asn Lys Leu Val	Cys Ser Gly Leu Leu Lys	
245	250	255
Leu Thr Lys Ala Asn Val Ile His Ala	Thr Val Thr Ser Val Thr	
260	265	270
Leu His Ser Thr Glu Gly Lys Ala Leu	Tyr Gln Val Ala Tyr Glu	
275	280	285
Asn Glu Val Gly Asn Ser Ser Asp Phe	Tyr Asp Ile Val Val Ile	
290	295	300
Ala Thr Pro Leu His Leu Asp Asn Ser	Ser Ser Asn Leu Thr Phe	
305	310	315
Ala Gly Phe His Pro Pro Ile Asp Asp	Val Gln Gly Ser Phe Gln	
320	325	330
Pro Thr Val Val Ser Leu Val His Gly	Tyr Leu Asn Ser Ser Tyr	
335	340	345
Phe Gly Phe Pro Asp Pro Lys Leu Phe	Pro Phe Ala Asn Ile Leu	
350	355	360
Thr Thr Asp Phe Pro Ser Phe Phe Cys	Thr Leu Asp Asn Ile Cys	
365	370	375
Pro Val Asn Ile Ser Ala Ser Phe Arg	Arg Lys Gln Pro Gln Glu	
380	385	390
Ala Ala Val Trp Arg Val Gln Ser Pro	Lys Pro Leu Phe Arg Thr	
395	400	405

Gln Leu Lys Thr Leu Phe Arg Ser Tyr Tyr Ser Val Gln Thr Ala  
410 415 420

Glu Trp Gln Ala His Pro Leu Tyr Gly Ser Arg Pro Thr Leu Pro  
425 430 435

Arg Phe Ala Leu His Asp Gln Leu Phe Tyr Leu Asn Ala Leu Glu  
440 445 450

Trp Ala Ala Ser Ser Val Glu Val Met Ala Val Ala Ala Lys Asn  
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Val Ala Leu Leu Ala Tyr Asn Arg Trp Tyr Gln Asp Leu Asp Lys  
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Ile Asp Gln Lys Asp Leu Met His Lys Val Lys Thr Glu Leu  
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